

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:52:21 / Search time 28 Seconds
(without alignments)
166.221 Million cell updates/sec

Title: US-09-759-112a-24
Perfect score: 582
Sequence: 1 DIVLTNSPALSIVSLGGRAT.....COLCNDPPPTFGAGTKLEIK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	537.5	92.4	132	2	US-08-483-636-2
2	537.5	92.4	132	2	US-08-483-632-2
3	519.5	89.3	111	1	US-08-491-845-8
4	516.5	88.7	131	3	US-08-579-378A-14
5	503.5	86.5	106	3	US-08-466-151-6
6	503.5	86.5	106	4	US-08-466-163B-6
7	491.5	84.5	111	3	US-08-466-151-2
8	491.5	84.5	111	4	US-08-466-163B-2
9	490.5	84.3	120	1	US-08-111-080-24
10	490.5	84.3	120	1	US-08-211-980-24
11	490.5	84.3	120	5	PCT-US93-07967-24
12	485.5	83.4	111	2	US-08-887-352B-5
13	485.5	83.4	111	2	US-09-109-207C-5
14	485.5	83.4	111	3	US-09-296-005-5
15	469.5	80.7	131	2	US-08-483-636-58
16	469.5	80.7	131	2	US-08-483-632-58
17	465.5	80.0	131	1	US-08-137-117D-33
18	465.5	80.0	131	2	US-08-436-717-33
19	463.5	79.6	131	2	US-08-483-636-14
20	463.5	79.6	131	2	US-08-483-632-14
21	460.5	79.1	131	2	US-08-137-117D-25
22	460.5	79.1	131	2	US-08-436-717-25
23	456.5	78.4	131	2	US-08-621-751A-10
24	453.5	77.9	111	1	US-08-275-053-11
25	453.5	77.9	121	1	US-08-111-080-22
26	453.5	77.9	121	1	US-08-211-980-22
27	453.5	77.9	121	5	PCT-US93-07967-22

28	449.5	77.2	111	2	US-08-483-636-73	Sequence 73, Appl
29	449.5	77.2	111	2	US-08-483-632-73	Sequence 73, Appl
30	448.5	77.1	129	4	US-09-556-605-2	Sequence 2, Appl1
31	447	76.8	151	4	US-09-318-786-33	Sequence 33, Appl
32	446.5	76.7	120	1	US-08-111-080-26	Sequence 26, Appl
33	446.5	76.7	120	1	US-08-211-980-26	Sequence 26, Appl
34	446.5	76.7	120	5	PCT-US93-07967-26	Sequence 26, Appl
35	444.5	76.4	111	1	US-08-207-169A-4	Sequence 4, Appl1
36	444.5	76.4	121	1	US-08-111-080-18	Sequence 18, Appl
37	444.5	76.4	121	1	US-08-211-980-18	Sequence 18, Appl
38	444.5	76.4	121	5	PCT-US92-07111-17	Sequence 17, Appl
39	444.5	76.4	121	5	PCT-US93-07967-18	Sequence 18, Appl
40	444	76.3	110	1	US-08-017-570-2	Sequence 2, Appl1
41	444	76.3	110	4	US-08-471-426-2	Sequence 2, Appl1
42	444	76.3	110	4	US-09-672-609-13	Sequence 13, Appl
43	444	76.3	110	4	US-09-025-403A-13	Sequence 13, Appl
44	444	76.3	110	5	PCT-US94-01709-2	Sequence 2, Appl1
45	439.5	75.5	132	2	US-08-379-057-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-2
Sequence 2, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-483-636-2

Query Match	92.48;	Score 537.5;	DB 2;	Length 132;
Best Local Similarity	93.78;	Pred. No. 2.2e-49;		
Matches 104; Conservative	1;	Mismatches 5;	Indels 1;	Gaps 1;

QY	QY	QY	QY
1	21	60	81
DIYLTNSPALAVSLGCRATISCKASQSDYDDEDSYW-WYOOKPGOPPKLITLYTAASNLSS	DIYLTQSPALAVSLGCRATISCKASQSDYDDEDSYMNMYGQKPGOPPKLITLYTAASNLSS	GIARPSGSSGSDFTLNTHPVEEDDAATYYCQLCEDNPPPTGAGKLEIK	GIARPSGSSGSDFTLNTHPVEEDDAATYYCQSNEDPPPTGEGKLEIK
59	800	110	131

RESULT 2
US-08-483-632-2
; Sequence 2, Application US/08483632
; Patent No. 5028004

GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,632
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993

APPLICATION NUMBER: PCT/US/94/10308
 FILING DATE: 07-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sulton, Jeffrey A.
 REGISTRATION NUMBER: 34,028
 REFERENCE/DOCKET NUMBER: P50186-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 270-5024
 TELEFAX: (215) 270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 OS-08-483-632-2

Query Match	92.4%;	Score 537.5;	DB 2;	Length 132;
Best Local Similarity	93.7%;	Pred. No. 2.2e-49;		
Matches 104; Conservative	1;	Mismatches 5;	Indels 1;	Gaps 1

QY 1 DIVLTNSPPLAVSLGCRATISCKASQVDYDDSYM-WYQOKPGQPKLLTYAASNLES 59

Db 21 DIVLTQSPASLAVSLGRATISCKASQSDVDYDGD SYMNWYQQKPGQP KLLIYAASNLES 80

Qy 60 GIPARFGSSSGTDFLTNIHPVEEDATYYCQLCNEDPPTFGAGTKLEK 110
| | | | | | | | | | | | | | | :
Db 81 GIPARFGSSGTDFTLNHPVEEDATYYCQSNEDPPTFGGCTKEIK 131

RESULT 3
US-08-491-845-8
; Sequence 8, Application US/08491845
; Patent No. 5773247

GENERAL INFORMATION:
APPLICANT: MAEDA, Hiroaki
APPLICANT: KITACHI, Kazuhiko
APPLICANT: EDA, Yasuyuki
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATO, Kiyoshi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 1

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP93/000399
 FILING DATE: 14-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Broadway, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: MAEDA=5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEFAX: (202) 757-3528
 INFORMATION FOR SEQ ID NO: 8:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-491-845-8

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Query Match	89.38;	Score 519.5;	DB 1;	Length 111;
Best Local Similarity	91.98;	Pred. No. 1.4e-47;		
Matches 102; Conservative	0;	Mismatches 8;	Indels 1;	Gaps 1;

[illegible]

RESULT: 4
US-08-579-378A-14
; Sequence 14, Application US/08579378A
; Patent No. 6210671
GENERAL INFORMATION:

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STATE California  
COUNTRY: USA  
ZIP: 94080  
  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 06-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/879495  
FILING DATE: 07-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P2CID1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NOS: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear
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US-08-466-151-6

	Query Match	Best Local Similarity	Matches	% Conservative	Score	SOC	ID NO:	DB	Length	Gaps
OY	I DIVLTNSPASLAVSLVSGQRATISCKASQSVDDGDSYM-WYQAKPGCPKLLTYAASNLES	93.4%	99	0	503.5	6	1	61	106	1
Dy	1 DVLDTGPSALVASLVSGRATISKASQSDVDGSYNWNYQAKPGCPKLLIYAASNLES							60		
OY	60 GIPIARESSGGSTDETLNINHVEEEDAAITYYCQLCNDFPTFGAGT							105		
Dy	61 GIPIARESSGGSTDETLNINHVEEEDDAATYYCCOQSNBDFPFAGT							106		

RESULT 6
US-08-466-163B-6
Sequence 6, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2CID1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-6

Query Match 86.5%; Score 503.5; DB 4; Length 106;
Best Local Similarity 93.4%; Pred. No. 6.4e-46;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSIGORATISCKRASOSVDYDGSYM-WYOOKPQOPKLLTYASNL5 59
DB 1 DIVLTQSPASTAVSIGORATISCKRASOSVDYDGSYMWYOOKPQOPKLLTYASNL5 60
QY 60 GIPARFSGSGGTDEFTLNHIVEEDATYTCOLCNEDEPPTFGAGTKLEK 105
DB 61 EIPARFSGSGGTDEFTLNHIVEEDATYTCOOSHEDPTFGAGTKLEK 106

ULT 7
US-08-466-151-2
Sequence 2, Application US/08466151
Patent No. 6037453

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPain (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-2

Query Match 84.5%; Score 491.5; DB 3; Length 111;

Best Local Similarity 88.3%; Pred. No. 1.2e-44;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSIGORATISCKRASOSVDYDGSYM-WYOOKPQOPKLLTYASNL5 59
DB 1 DIVLTQSPASTAVSIGORATISCKRASOSVDYDGSYMWYOOKPQOPKLLTYASNL5 60
QY 60 GIPARFSGSGGTDEFTLNHIVEEDATYTCOLCNEDEPPTFGAGTKLEK 110
DB 61 EIPARFSGSGGTDEFTLNHIVEEDATYTCOOSHEDPTFGAGTKLEK 111

RESULT 8
US-08-466-163B-2
Sequence 2, Application US/08466163B
Patent No. 6329509

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 2

LENGTH: 111
TYPE: PRT
ORGANISM: Mus musculus
US-08-466-163B-2

Query Match 84.5%; Score 491.5; DB 4; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.2e-44;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSIGORATISCKRASOSVDYDGSYM-WYOOKPQOPKLLTYASNL5 59
DB 1 DIVLTQSPASTAVSIGORATISCKRASOSVDYDGSYMWYOOKPQOPKLLTYASNL5 60
QY 60 GIPARFSGSGGTDEFTLNHIVEEDATYTCOLCNEDEPPTFGAGTKLEK 110
DB 61 EIPARFSGSGGTDEFTLNHIVEEDATYTCOOSHEDPTFGAGTKLEK 111

RESULT 9
US-08-111-080-24
Sequence 24, Application 08/111080
Patent No. 5558665

GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/111,080
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-111-080-24

Query Match 84.3%; Score 490.5; DB 1; Length 120;
Best Local Similarity 87.3%; Pred. No. 1.7e-44;
Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASIYSLGQRTATSCASOSVDYDGSYM-WYQKRGQPKLLTYASNL 59
DB 1 DIVLTQSPASLAVSLGQRTATSCASOSVDYDGSYMMWYQKRGQPKLLTYASNVES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQLCNEDPPTFGAGTKLEL 109
DB 61 GIPARFYGSGGTDFTNTHPVEEEDATYYCQGSIDDPSTFGGKTLEI 110

RESULT 10
US-08-211-980-24
Sequence 24, Application US/08211980
Patent No. 5665569
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/211,980
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-980-24

Query Match 84.3%; Score 490.5; DB 1; Length 120;
Best Local Similarity 87.3%; Pred. No. 1.7e-44;
Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASIYSLGQRTATSCASOSVDYDGSYM-WYQKRGQPKLLTYASNL 59
DB 1 DIVLTQSPASLAVSLGQRTATSCASOSVDYDGSYMMWYQKRGQPKLLTYASNVES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQLCNEDPPTFGAGTKLEL 109
DB 61 GIPARFYGSGGTDFTNTHPVEEEDATYYCQGSIDDPSTFGGKTLEI 110

RESULT 11
PCT-US93-07967-24
Sequence 24, Application PC/US9307967

GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/07967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-07967-24


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1 STATE: PA
2 COUNTRY: USA
3 ZIP: 19406-0939
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: PatentIn Release #1.0, Version #1.25Z
10
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/483,636
13 FILING DATE:
14
15 CLASSIFICATION: 424
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/117366
19 FILING DATE: 07-SEP-1993
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 08/136783
23 FILING DATE: 14-OCT-1993
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: PCT/US/94/10308
27 FILING DATE: 07-SEP-1994
28
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Sulton, Jeffrey A.
31 REGISTRATION NUMBER: 34,028
32 REFERENCE/DOCKET NUMBER: P50186-3
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (215) 270-5024
35 TELEFAX: (215) 270-5090
36
37 INFORMATION FOR SEQ ID NO: 58:
38
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 131 amino acids
41 TYPE: amino acid
42 TOPOLOGY: linear
43
44 MOLECULE TYPE: protein
45
46 OS-08-483-636-58

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Query Match	80.7%	Score 469.5	DB 2	Length 131
Best Local Similarity	80.2%	Pred. No. 3.1e-42		
Matches 89	Conservative	8	Mismatches 13	Indels 1
				Gaps 1

[illegible]

Search completed: September 13, 2003, 07:56:02
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2003, 06:42:50 : Search time 74 Seconds
(without alignments)
235.945 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582
Sequence: 1 DVLVFNPSLAWSLGGRAF.....COLCNDPPPTFGAGTKLELK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	110	23	AAO18536 Murine Mab 1F7 lig
2	537.5	92.4	132	16	AA870189 Mouse Mab 3B9 lig
3	537.5	92.4	132	20	AA123767 Light chain variab
4	537.5	92.4	132	20	AA18120 Light chain sequen
5	532.5	91.5	111	21	AA59267 Antibody 4H5 L cha
6	532.5	91.5	111	21	AA51144 Murine derived pro
7	532.5	91.5	111	21	AA51146 Murine derived pro
8	532.5	91.5	305	21	AA59264 Antibody 4H5 H cha
9	532.5	91.5	305	21	AA59265 Antibody 4H5 L cha

10	532.5	91.5	305	21	AA51141 Murine derived pro
11	532.5	91.5	305	21	AA51142 Murine derived pro
12	528.5	90.8	238	19	AA83042 Anti-Fas Mab HEF7A
13	528.5	90.8	238	21	AA14748 Mouse anti-Fas ant
14	528.5	90.8	238	21	AAW90898 Murine anti-Fas an
15	528.5	90.8	238	23	AA874867 Humanised anti-Fas
16	528.5	90.8	238	23	AA874913 Humanised anti-Fas
17	526.5	90.5	238	23	AAE18371 Human penton base
18	526.5	90.5	238	24	ABG76346 Mouse DAV-1 light
19	522.5	89.8	111	15	AA855123 Mouse anti-HIV mu5
20	522.5	89.8	111	15	AA860302 Anti HIV antibody
21	521.5	89.6	131	14	AA832123 Anti-CD4 antibody
22	519.5	89.3	111	10	AA890541 Immunoglobulin L c
23	519.5	89.3	111	10	AAU99852 Mouse AC10 antibody
24	519.5	89.3	131	10	AA890543 Amino acids sequen
25	515.5	88.6	113	22	AA871895 Monoclonal antibod
26	512.5	88.1	122	18	AAW01751 MHI monoclonal ant
27	511.5	87.9	131	11	AA804132 Anti-Leu 3a light
28	503.5	86.5	106	14	AA833309 MAE15 light chain.
29	503.5	86.5	106	21	AA85197 Light chain amino
30	503.5	86.5	112	22	AA862872 Anti-SAF-1 monoclo
31	498.5	85.7	103	21	AA59263 Antibody 4H5 L cha
32	498.5	85.7	103	21	AA51140 Murine derived pro
33	491.5	84.5	111	14	AA833305 MAE11 light chain.
34	491.5	84.5	111	21	AA85193 Light chain amino
35	490.5	84.3	120	15	AA848618 Sequence of the mo
36	487.5	83.8	218	15	ABP96773 TSH receptor antib
37	487.5	83.8	218	24	ABP96774 Anti-Fas humanised
38	487.5	83.8	238	19	AAW83033 Humanised anti-Fas
39	487.5	83.8	238	21	AA814774 Humanised anti-Fas
40	487.5	83.8	238	21	AAW90924 Humanised anti-Fas
41	487.5	83.8	238	23	AB874893 Humanised anti-Fas
42	487.5	83.8	238	23	AB874839 Humanised anti-Fas
43	485.5	83.4	111	20	AAW95650 Mus musculus anti-
44	485.5	83.4	111	20	AA876939 Variable light cha
45	476.5	81.9	238	19	AAW83032 Anti-Fas humanised

ALIGNMENTS

RESULT 1	
AAO18536	AAO18536 standard; Protein; 110 AA.
ID	AAO18536
XX	AAO18536;
AC	AAO18536;
XX	11-OCT-2002 (first entry)
DT	11-OCT-2002 (first entry)
XX	
DE	Murine Mab 1F7 light chain.
XX	
KW	Mouse: 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
KW	complementarity determining region; framework-determining region;
KW	FR; heavy chain; light chain; HIV infection.
XX	
OS	Mus sp.
XX	
PN	W0200255668-A2.
XX	18-JUL-2002.
PD	
XX	11-JAN-2002; 2002WO-US00927.
PE	
XX	11-JAN-2001; 2001US-0759112.
PR	
XX	(IMMP-) IMMPPERON INC.
PA	
XX	Muller S, Kohler H;
PI	
XX	WPI; 2002-590668/63.
DR	N-PSDB; AAL48661.
XX	
PT	New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate
 PT anti-human immunodeficiency virus (HIV) antibodies, for use in
 PT vaccines against HIV -

XX Claim 9: page 23-24; 27pp; English.

CC The present invention relates to coding sequences of the murine 1F7
 CC anti-idiotypic antibody complementarity-determining region (CDR) or
 CC framework-determining region (FR). The antibody binds to human or primate
 CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the
 CC treatment of HIV infection. The present sequence is the 1F7 light chain.

XX Sequence 110 AA:

Query Match 100.0%; Score 582; DB 23; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.3e-42;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIVLTNSPASPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLSESG 60
 1 DIVLTNSPASPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLSESG 60
 DB 61 IPARFSGSGSGTDFLTNTHPVEEDAAATYYCOLCNEDEPPTFGAGTKLELK 110
 61 IPARFSGSGSGTDFLTNTHPVEEDAAATYYCOLCNEDEPPTFGAGTKLELK 110

RESULT 2

ID AAR70189 standard; Protein; 132 AA.

XX AAR70189;

DT 25-MAR-2003 (updated)
 DT 20-SEP-1995 (first entry)

XX Mouse Mab 3B9 light chain.

KW Chimeric antibody; humanized antibody; antibody engineering;
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Region /label= Sig_peptide 44..58

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

FT Region /label= CDR /note= "complementarity determining region"

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IGE-mediated allergic conditions

XX Disclosure; Fig.1; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (AA083490-91), and used for
 CC antibody engineering
 CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 132 AA:

Query Match 92.4%; Score 537.5; DB 16; Length 132;
 Best Local Similarity 93.7%; Pred. No. 1e-38;
 Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

OY 1 DIVLTNSPASPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLSESG 59
 21 DIVLTNSPASPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLSESG 60
 DB 60 GIPARFSGSGSGTDFLTNTHPVEEDAAATYYCOLCNEDEPPTFGAGTKLELK 110
 81 GIPARFSGSGSGTDFLTNTHPVEEDAAATYYCOLCNEDEPPTFGAGTKLELK 131

RESULT 3

ID AAY23767 standard; Protein; 132 AA.

XX AAY23767;

DT 13-SEP-1999 (first entry)

XX Light chain variable region of murine IL-4 antibody 3B9.

KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanized antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy.

XX Mus sp.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1995; 95US-0483632.

XX 07-SEP-1995; 95US-0483632.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX Gross MS, Holmes SD, Sylvester DR;

XX Gross MS, Holmes SD, Sylvester DR;

XX Gross MS, Holmes SD, Sylvester DR;

XX Gross MS, Holmes SD, Sylvester DR;

XX Gross MS, Holmes SD, Sylvester DR;

XX Gross MS, Holmes SD, Sylvester DR;

XX The present sequence represents the light chain variable region of

CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
CC in the production chimeric and humanised IL-4 monoclonal antibodies.
CC The antibodies of the invention are used in therapeutic and
CC pharmaceutical compositions for treating IL-4 mediated and
CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
CC rheumatoid arthritis, host-versus-graft disease and renal disease.
CC They are also useful in the diagnosis of an allergy or condition
CC associated with excess IL-4 production through the measurement e.g. by
CC ELISA of circulating endogenous IL-4 levels in humans.

Query Match	92.4%	Score 537.5	DB 20	Length 132
Best Local Similarity	93.7%	Pred. No. 1e-38		
Matches 104	Conservative 1	Mismatches 5	Indels 1	Gaps 1

CC and as such are useful in the treatment of autoimmune diseases and graft CC versus host disease.

Query Match	92.4%	Score 537.5	DB 20	Length 132
Best Local Similarity	93.7%	Pred. No. 1e-38		
Matches 104	Conservative 1	Mismatches 5	Indels 1	Gaps 1

Query Match	91.5%	Score 532.5	DB 21	Length 111
Best Local Similarity	92.8%	Pred. No. 2.3e-38		
Matches 103; Conservative	2	Mismatches 5	Indels 1	Gaps 1

AC AAV51144;
 XX 31-MAR-2000 (first entry)
 DT
 XX Murine derived protein fragment #6.
 DE
 XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KM hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KM HIV infection; autoimmune disease; murine.
 XX
 OS Mus sp.
 PN W09961629-A1.
 XX
 XX 02-DEC-1999.
 PD
 XX 24-MAY-1999; 99WO-JP02711.
 PE
 XX 25-MAY-1998; 98JP-0159957.
 PR 26-MAY-1998; 98JP-0163023.
 XX
 XX (ASAHI) ASAH I KASEI KOGYO KK.
 XX (ASAHI) ASAH I MEDICAL CO LTD.
 XX
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 DR WPI: 2000-086720/07.
 XX
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 XX
 PS Disclosure: Page 95; 111pp; Japanese.
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 CC
 SQ Sequence 111 AA:
 Query Match 91.5%; Score 532.5; DB 21; Length 111;
 Best Local Similarity 92.8%; Pred. No. 2.3e-38;
 Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 DB 1 DIVLTNSPASLAVSLGQRATISCKASQSVVDYDGSYM-WYQOKPGQPKLLTYAASNLES 59
 1 DIVLTGSPASLAVSLGQRATISCKASQSVVDYDGSYMMWYQOKPGQPKLLTYAASNLES 60
 QY 60 GIPARFSSGSGTDTFTLNHIVEEDATYYCQLCNEDEPPTFGAGTKLELK 110
 61 GIPARFSSGSGTDTFTLNHIVEEDATYYCQSSSEDPPTFGGCTKLEIK 111
 DB
 RESULT 7
 AAV51146
 ID AAV51146 standard; Protein: 111 AA.
 XX
 AC AAV51146;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 XX Murine derived protein fragment #8.
 DE
 XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KM hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KM HIV infection; autoimmune disease; murine.
 XX

OS Mus sp.
 XX W09961629-A1.
 XX
 XX 02-DEC-1999.
 PD
 XX 24-MAY-1999; 99WO-JP02711.
 PE
 XX 25-MAY-1998; 98JP-0159957.
 PR 26-MAY-1998; 98JP-0163023.
 XX
 XX (ASAHI) ASAH I KASEI KOGYO KK.
 XX (ASAHI) ASAH I MEDICAL CO LTD.
 XX
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 DR WPI: 2000-086720/07.
 DR N-PSDB: AA244232.
 XX
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 XX
 PS Disclosure: Page 97-98; 111pp; Japanese.
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 CC
 SQ Sequence 111 AA:
 Query Match 91.5%; Score 532.5; DB 21; Length 111;
 Best Local Similarity 92.8%; Pred. No. 2.3e-38;
 Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 DB 1 DIVLTNSPASLAVSLGQRATISCKASQSVVDYDGSYM-WYQOKPGQPKLLTYAASNLES 59
 1 DIVLTGSPASLAVSLGQRATISCKASQSVVDYDGSYMMWYQOKPGQPKLLTYAASNLES 60
 QY 60 GIPARFSSGSGTDTFTLNHIVEEDATYYCQLCNEDEPPTFGAGTKLELK 110
 61 GIPARFSSGSGTDTFTLNHIVEEDATYYCQSSSEDPPTFGGCTKLEIK 111
 DB
 RESULT 8
 AAV51264
 ID AAV51264 standard; Protein: 305 AA.
 XX
 AC AAV51264;
 XX
 DT 17-APR-2000 (first entry)
 XX
 XX Antibody 4H5 H chain sequence.
 DE
 XX CD4 antigen; anti-human; antibody; 4H5; drug.
 KM
 XX Mus sp.
 OS
 XX JPL1332563-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 26-MAY-1998; 98JP-0163034.
 PE
 XX 26-MAY-1998; 98JP-0163034.
 PR
 XX (ASAHI) ASAH I KASEI KOGYO KK.
 XX


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XX AAV51142;
AC 31-MAR-2000 (first entry)
XX Murine derived protein fragment #4.
DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KM HIV infection; autoimmune disease; murine.
XX Mus sp.
OS WO9961629-A1.
XX 02-DEC-1999.
XX 24-MAY-1999; 99WO-JP02711.
XX 25-MAY-1998; 98JP-0159957.
XX 26-MAY-1998; 98JP-0163023.
XX (ASAH ) ASAH KASEI KOCYO KK.
XX (ASAH ) ASAH MEDICAL CO LTD.
XX Ono M, Soka T, Morimoto I, Miyamura K;
XX WPI: 2000-086720/07.
XX N-PSDB: AA244206.
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells
XX Claim 22; Page 82-84; 11pp; Japanese.
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.
XX Sequence 305 AA;
XX Query Match 91.5%; Score 532.5; DB 21; Length 305;
XX Fast Local Similarity 92.8%; Pred. No. 6.3e-38;
XX Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
XX 1 DIVLTNSPASIYAVSGORATISCKASOSVDYDGSYM-WYOOKPGOPKLLTYASNLS 59
XX 156 DIVLTQSPASIVASIGORATISCKASQSVDYDGSYMMWYOOKPGOPKLLTYASNLS 215
XX 60 GIPARFSGSGGTFTLTNIHPEVEEDATYYCOLCNEPPTFGAAGTKLEIK 110
XX 216 GIPARFSGSGGTFTLTNIHPEVEEDATYYCQOSEEDPPTFGAAGTKLEIK 266
XX
XX RESULT 12
XX AAW83042
XX ID AAW83042 standard; Protein; 238 AA.
XX AC AAW83042;
XX 25-MAR-2003 (updated)
XX 15-MAR-1999 (first entry)
XX Anti-Fas MAb HFE7A light chain.
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

```

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KM apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KM systemic lupus erythematosus; graft versus host disease;
KM Sjogren syndrome; pernicious anaemia; Addison's disease;
KM scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KM rheumatoid arthritis; autoimmune haemolytic anaemia;
KM myasthenia gravis; multiple sclerosis; Basedow's disease;
KM thrombopenia purpura; insulin-dependent diabetes; allergy;
KM atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KM glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KM transplant rejection; therapy; complementarity determining region;
KM CDR.
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX Protein /label= Sig_peptide
XX Region /label= Mat_protein
XX Region 21..131
XX Region /label= Variable
XX Region /label= Constant
XX Region /label= CDR_L1
XX Region /label= CDR_L2
XX Region /label= CDR_L3
XX Region /note= "claim 9"
XX Region /note= "claim 9"
XX Region /note= "claim 9"
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XX Region /note= "claim 9"
XX
XX AU9859701-A.
XX 08-OCT-1998.
XX 30-MAR-1998; 98AU-0059701.
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX (SANY ) SANKYO CO LTD.
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Rohru T;
XX WPI: 1998-543440/01.
XX N-PSDB: AAV70130.
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX Reference Example 4; Page 189-190; 292pp; English.
XX This is the amino acid of the light chain of murine anti-human Fas
XX monoclonal antibody HFE7A. cDNA (see AAV70130) encoding the light
XX chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
XX RNA by RT-PCR (see AAV70127-28). The invention provides humanised
XX HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These
XX antibodies are capable of inducing apoptosis in abnormal cells
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX cells. They are used to evaluate, in animal models, treatments of
XX diseases that involve Fas/Fas ligand interactions, and also to treat
XX such diseases, including autoimmune disease (e.g. systemic lupus
XX erythematosus, Hashimoto's disease, graft versus host disease,
XX Sjogren syndrome, pernicious anaemia, Addison's disease,
XX scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
XX arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
XX gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura

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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:50:50 ; Search time 37 Seconds
(Without alignments)
285.907 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582

Sequence: 1 DIVLTNPSASLAVSLGCRAT.....COLCNEPPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533.5	91.7	111	1	KVMS83
2	527.5	90.6	111	1	KVMS43
3	523.5	89.9	111	1	KVMS08
4	521.5	89.6	112	2	S19971
5	521.5	89.6	131	2	PH1226
6	520.5	89.4	111	1	KVMS69
7	505	86.8	110	1	KVMS10
8	503.5	86.5	111	1	KVMS01
9	502.5	86.3	112	2	S19976
10	485.5	83.4	112	2	S19972
11	476.5	81.9	111	1	S09966
12	473.5	81.4	111	1	KVMS75
13	470.5	80.8	111	1	KVMS40
14	468.5	80.5	111	1	KVMS84
15	457.5	78.6	112	2	S45715
16	455.5	78.3	111	1	KVMS37
17	454.5	78.1	111	1	KVMS85
18	452.5	77.7	131	2	S55027
19	451.5	77.6	210	2	A56169
20	449.5	77.2	218	2	JCS810
21	448.5	77.1	131	1	KVMSM6
22	445.5	76.5	218	2	S68241
23	442.5	76.0	115	2	S63596
24	441.5	75.9	93	2	A38601
25	438.5	75.3	111	2	S09963
26	438.5	75.3	111	2	D45722
27	432.5	74.3	111	1	KVMS80
28	430.5	74.0	107	2	S26343
29	430.5	74.0	107	2	S26344

30	430.5	74.0	108	1	KVMS54	Ig kappa chain V r
31	429.5	73.8	111	2	PL0081	Ig kappa chain V r
32	428.5	73.6	111	1	KVMS50	Ig kappa chain V r
33	428	73.5	110	2	S24288	Ig kappa chain V r
34	427.5	73.3	111	2	S09969	Ig kappa chain V-J
35	426.5	73.3	140	2	PN0446	Ig kappa chain pre
36	424.5	72.9	132	1	KVMS32	Ig kappa chain pre
37	421.5	72.4	111	2	S09965	Ig kappa chain V-J
38	417.5	71.7	102	2	PH1076	Ig light chain V r
39	417	71.6	108	2	PH0092	Ig kappa chain V r
40	415.5	71.4	109	2	PH0093	Ig kappa chain V r
41	415.5	71.4	111	2	E53285	Ig kappa chain V r
42	410	70.4	233	2	EC5322	Ig kappa chain V a
43	405.5	69.7	102	2	PH1077	p53 specific singl
44	405.5	69.7	102	2	PH1079	Ig light chain V r
45	403.5	69.3	111	2	S37202	Ig light chain V r

ALIGNMENTS

RESULT 1

KVMS83
Ig kappa chain V region (PC7183) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000

C:Accession: B01937; A01937

R:Weigert, M.; Galtaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: B01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin homology <IMM>

F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 91.7%; Score 533.5; DB 1; Length 111;
Best Local Similarity 94.6%; Pred. No. 2.6e-41;

Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNPSASLAVSLGCRATISCKASQSDYDGDSTW-WYQKPGQPKLLTYAASNLBS 59

Db 1 DIVLTQSPASLAVSLGCRATISCKASQSDYDGDSTWYQKPGQPKLLTYAASNLBS 60

QY 60 GIPARFSGSGGCTFTLNTHPVEEDDAATYYCOLEDDPPTFGAGTKLELK 110

Db 61 GIPARFSGSGGCTFTLNTHPVEEDDAATYYCOLEDDPPTFGAGTKLELK 111

RESULT 2

KVMS43
Ig kappa chain V region (PC7043) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000

C:Accession: A01937; S42187; S42190; S42189; S42188; S42191; S42192

R:Weigert, M.; Galtaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: A01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42187

A:Molecule type: DNA

Matches 100; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGQPKLLTYAASNLES 59

Db 21 DIVLTGSPASLAVSLGQRATISCKASOSLDYDSDSYNMYQKPGQPKLLTYAASNLES 80

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 81 GIPARFSGSGGTDFTLNHPVEEDAAATYCCQSSDEPTFGGTRLEIK 131

RESULT 6

KVMS69

Ig kappa chain V region (PC7769) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000

C:Accession: E01937; A01937

R:Weigert, M.; Galtmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Title: Rearrangement of genetic information may produce immunoglobulin diversity.

Reference number: A93204; MUID:79073152; PMID:103003

Accession: E01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 89.4%; Score 520.5; DB 1; Length 111;

Best Local Similarity 91.0%; Pred. No. 3.8e-40;

Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGQPKLLTYAASNLES 59

Db 1 DIVLTGSPASLAVSLGQRATISCKASOSVDYDSDSYNMYQKPGQPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 61 GIPARFSGSGGTDFTLNHPVEEDAAATYCCQSSDEPTFGGTRLEIK 111

RESULT 7

KVMS10

Ig kappa chain V region (PC7210) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000

C:Accession: D01937; A01937

R:Weigert, M.; Galtmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Title: Rearrangement of genetic information may produce immunoglobulin diversity.

Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: D01937

A:Molecule type: protein

A:Residues: 1-110 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 86.8%; Score 505; DB 1; Length 110;

Best Local Similarity 90.1%; Pred. No. 9.4e-39;

Matches 100; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGQPKLLTYAASNLES 59

Db 1 DIVLTGSPASLAVSLGQRATISCKASOSLDYDSDSYNMYQKPGQPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 61 GIPARFSGSGGTDFTLNHPVEEDAAATYCCQSSDEPTFGGTRLEIK 110

RESULT 8

KVMS1

Ig kappa chain V region (CAPC 101) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000

C:Accession: A01936

R:McKean, D.J.; Bell, M.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related

A:Reference number: A93822; MUID:79012520; PMID:99744

A:Accession: A01936

A:Molecule type: protein

A:Residues: 1-111 <MCK>

C:Comment: This chain was isolated from a myeloma protein.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 86.5%; Score 503.5; DB 1; Length 111;

Best Local Similarity 89.2%; Pred. No. 1.3e-38;

Matches 99; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGQPKLLTYAASNLES 59

Db 1 DIVLTGSPASLAVSLGQRATISCKASOSVDYDSDSYNMYQKPGQPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 61 GIPARFSGSGGTDFTLNHPVEEDAAATYCCQSSDEPTFGGTRLEIK 111

RESULT 9

S19976

Ig kappa chain V region (M-T413) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C:Accession: S19976

R:Weissenborn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mab.

A:Reference number: S19963

A:Accession: S19976

A:Molecule type: preliminary

A:Residues: 1-112 <WEI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 502.5; DB 2; Length 112;

Best Local Similarity 88.3%; Pred. No. 1.6e-38;

Matches 98; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASOSVDYDSDSYN-WYQKPGQPKLLTYAASNLES 59

Db 1 DIVLTGSPASLAVSLGQRATISCKASOSLDYDSDSYNMYQKPGQPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYCCOLCNEDEPTFGAGTKLEIK 110

Db 61 GIPARFSGSGGTDFTLNHPVEEDAAATYCCQSSIDDPYTFGGTRLEIK 111

RESULT 10

S19972

Ig kappa chain V region (M-T321) - mouse (fragment)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:45:09 ; Search time 23 Seconds
(without alignments)
224.910 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582

Sequence: 1 DIVLTNSPASTAVSLGQRAT.....COLCNEPPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533.5	91.7	111	1	KV3N_MOUSE
2	527.5	90.6	111	1	KV3M_MOUSE
3	523.5	89.9	111	1	KV3O_MOUSE
4	520.5	89.4	111	1	KV3O_MOUSE
5	505	86.8	110	1	KV3L_MOUSE
6	503.5	86.5	111	1	KV3L_MOUSE
7	473.5	81.4	111	1	KV3S_MOUSE
8	470.5	80.8	111	1	KV3R_MOUSE
9	468.5	80.5	111	1	KV3R_MOUSE
10	455.5	78.3	111	1	KV3K_MOUSE
11	455.5	78.3	111	1	KV3K_MOUSE
12	454.5	78.1	111	1	KV3U_MOUSE
13	449.5	77.2	111	1	KV3I_MOUSE
14	448.5	77.1	111	1	KV3I_MOUSE
15	435.5	74.8	111	1	KV3C_MOUSE
16	433	74.4	112	1	KV3B_MOUSE
17	432.5	74.3	111	1	KV3A_MOUSE
18	430.5	74.0	108	1	KV3Y_MOUSE
19	428.5	73.6	111	1	KV3D_MOUSE
20	424.5	72.9	112	1	KV3G_MOUSE
21	424.5	72.9	112	1	KV3F_MOUSE
22	392.5	67.4	111	1	KV3E_MOUSE
23	373.5	64.2	114	1	KV4A_MOUSE
24	371.5	63.8	134	1	KV4C_MOUSE
25	366	62.9	133	1	KV4B_MOUSE
26	352.5	60.6	108	1	KV5P_MOUSE
27	351	60.3	129	1	KV3H_HUMAN
28	350.5	60.2	108	1	KV1M_HUMAN
29	344	59.1	109	1	KV3D_HUMAN
30	343	58.9	129	1	KV3L_HUMAN
31	340	58.4	109	1	KV3F_HUMAN
32	339	58.2	109	1	KV3B_HUMAN
33	337.5	58.0	108	1	KV1K_HUMAN

ALIGNMENTS

RESULT 1	ID	KV3N_MOUSE	STANDARD:	PRT:	111 AA.
AC	P01666:	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, last annotation update)				
DE	Ig kappa chain V-II region PC 7183.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=79073152; PubMed=103003;				
RA	Wiegert M, Gattaman L, Ioh E, Schilling J, Hood L.E.				
RT	"Rearrangement of genetic information may produce immunoglobulin				
RT	diversity."				
RL	Nature 276:785-790(1978).				
DR	PIR; B01937; KWS83.				
DR	HSSP: P01679; 2FBJ.				
DR	InterPro: IPR007110; Ig-like.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	PIfam: PF00047; Ig_1.				
DR	SMART: SM00406; IgV_1.				
DR	PROSITE: PS50835; IG_LIKE: 1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 23				
FT	DOMAIN 24 38				
FT	DOMAIN 39 53				
FT	DOMAIN 54 60				
FT	DOMAIN 61 92				
FT	DOMAIN 93 101				
FT	DOMAIN 102 111				
FT	DISULFID 23 92				
FT	NON_TER 111 111				
SO	SEQUENCE 111 AA; 11952 MW; 2058BB50CE306031 CRC64;				
Query Match	91.7%;	Score 533.5;	DB 1;	Length 111;	
Best Local Similarity	94.6%;	Pred. No. 1.8e-46;			
Matches 105;	Conservative 0;	Mismatches 5;	Indels 1;	Gaps 1;	
OY	1 DIVLTNSPASTAVSLGQRATISCKASQSVYDSDSYW-WYQOKPGOPPKLITYAASNLDS 59				
DB	1 DIVLTNSPASTAVSLGQRATISCKASQSVYDSDSYW-WYQOKPGOPPKLITYAASNLDS 60				
OY	60 GIDARPSGSGSDFTLNHPVEEDDAATYVYCOLCNEPPTFGAGTKLELK 110				
DB	61 GIDARPSGSGSDFTLNHPVEEDDAATYVYCOLCNEPPTFGAGTKLELK 111				
RESULT 2					
KV3M_MOUSE	STANDARD;	PRT;	111 AA.		
ID	P01665;				

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DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 7043.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR: A01937; KWS43.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 53 FRAMEWORK-2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 92 FRAMEWORK-3.
FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 101 FRAMEWORK-4.
FT DISULFID 102 111 BY SIMILARITY.
FT NON_TER 23 92
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 90.6%; Score 527.5; DB 1; Length 111;
Best Local Similarity 92.8%; Pred. No. 7.2e-46;
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

OY 1 DIVLTNSPASLAVSIGORATISCKASQSVYDGDSDYM-WYQOKPGQPKLLTYAASNLES 59
DB 1 DIVLTQSPASLAVSIGORATISCKASQSVYDGDSDYMMWYQOKPGQPKLLTYAASNLES 60
OY 60 GIPARFSSGSGTDFTLNHPVEEDAAATYYCQLCNEDPPFTGAGTKLEK 110
DB 61 GIPARFSSGSGTDFTLNHPVEEDAAATYYCQSNEDPFTGSGTKLEIK 111

MULT 3
O-MOUSE STANDARD: PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 6308.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR: C01937; KWS08.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR PIR: PF00047; Ig: 1.

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DR SMART; SM00406; IGV: 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 53 FRAMEWORK-2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 92 FRAMEWORK-3.
FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 101 FRAMEWORK-4.
FT DISULFID 102 111 BY SIMILARITY.
FT NON_TER 23 92
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 89.9%; Score 523.5; DB 1; Length 111;
Best Local Similarity 91.9%; Pred. No. 1.8e-45;
Matches 102; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

OY 1 DIVLTNSPASLAVSIGORATISCKASQSVYDGDSDYM-WYQOKPGQPKLLTYAASNLES 59
DB 1 DIVLTQSPASLAVSIGORATISCKASQSVYDGDSDYMMWYQOKPGQPKLLTYAASNLES 60
OY 60 GIPARFSSGSGTDFTLNHPVEEDAAATYYCQLCNEDPPFTGAGTKLEK 110
DB 61 GIPARFSSGSGTDFTLNHPVEEDAAATYYCQSNEDPFTGSGTKLEIK 111

RESULT 4
KV3Q_MOUSE STANDARD: PRT; 111 AA.
ID KV3Q_MOUSE
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 7769.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR: F01937; KWS69.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 53 FRAMEWORK-2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 92 FRAMEWORK-3.
FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 101 FRAMEWORK-4.
FT DISULFID 102 111 BY SIMILARITY.
FT NON_TER 23 92
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 89.4%; Score 520.5; DB 1; Length 111;
Best Local Similarity 91.0%; Pred. No. 3.6e-45;
Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

OY 1 DIVLTNSPASLAVSIGORATISCKASQSVYDGDSDYM-WYQOKPGQPKLLTYAASNLES 59
DB 1 DIVLTQSPASLAVSIGORATISCKASQSVYDGDSDYMMWYQOKPGQPKLLTYAASNLES 60

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OY 60 GIPARFSGSGTDFLTINHPVEEDATATYCCOLCNEPPTFGAGTKLEIK 110
 DB 61 GIPARFSGSGTDFLTINHPVEEDATATYCCOQSNEDPMTFGGKTLEIK 111

RESULT 5

KV3P_MOUSE STANDARD; PRT; 110 AA.
 AC P01668;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7210.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]

SEQUENCE.

MEDLINE=79073152; PubMed=103003;
 Weigert M., Gattalitan L., Loh E., Schilling J., Hood L.E.;
 "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 Nature 276:785-790(1978).
 RL Nature 276:785-790(1978).
 DR PIR: D01937; KVMSC1.
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_Like; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 101 110 FRAMEWORK-4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE8661249 CRC64;

Query Match 86.8%; Score 505; DB 1; Length 110;
 Best Local Similarity 90.1%; Pred. No. 1.2e-43;
 Matches 100; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

DB 1 DIVLTNSPASTAVSLGGRATISCKASQSVYDGDSDVM-WYQKRGCPKLLTYAASLLES 59
 1 DIVLTQSPASLAVSLGGRATISCKASQSLDYDGSINMWNWQKRGCPKLLTYAASLLES 60
 OY 60 GIPARFSGSGTDFLTINHPVEEDATATYCCOLCNEPPTFGAGTKLEIK 110
 DB 61 GIPARFSGSGTDFLTINHPVEEDATATYCCOQSNEDPMTFGGKTLEIK 110

RESULT 6

KV3L_MOUSE STANDARD; PRT; 111 AA.
 AC P01664;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region CBPC 101.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE.
 MEDLINE=79012520; PubMed=99744;

RA McKean D.J., Bell M., Potter M.;
 "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions";
 RT Proc. Natl. Acad. Sci. U.S.A. 73:3913-3917(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR: A01936; KVMSC1.
 DR HSSP: P80362; 1WTL.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_Like; 1.
 KM Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 111 FRAMEWORK-4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11964 MW; EZBIAD98AD965962 CRC64;

Query Match 86.5%; Score 503.5; DB 1; Length 111;
 Best Local Similarity 89.2%; Pred. No. 1.8e-43;
 Matches 99; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

OY 1 DIVLTNSPASTAVSLGGRATISCKASQSVYDGDSDVM-WYQKRGCPKLLTYAASLLES 59
 DB 1 DIVLTQSPASLAVSLGGRATISCKASQSVYTGESINMWNWQKRGCPKLLTYAASLLES 60
 OY 60 GIPARFSGSGTDFLTINHPVEEDATATYCCOLCNEPPTFGAGTKLEIK 110
 DB 61 GIPARFSGSGTDFLTINHPVEEDATATYCCOQSNEDPMTFGGKTLEIK 111

RESULT 7

KV3S_MOUSE STANDARD; PRT; 111 AA.
 AC P01671;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7175.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE.
 MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gattalitan L., Loh E., Schilling J., Hood L.E.;
 "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 Nature 276:785-790(1978).
 RL Nature 276:785-790(1978).
 DR PIR: B01938; KVMSC1.
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_Like; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 111 FRAMEWORK-4.

FT DISULEID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 81.4%; Score 473.5; DB 1; Length 111;
 Best Local Similarity 85.8%; Pred. No. 1.7e-40;
 Matches 95; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASQSYVDGDSYM-WYQKPGQPKLLTYAASNLSS 59
 DB 1 DIVLTQSPASLAVSLGQRATISCKRASKSVSTSGYSYMHMYQKPGQPKLLTYLASNLSS 60
 QY 60 GIPARFSGSGSGTDFLTNIHPVEEEDATYYCOLCNEPPTGAGTKLELK 110
 DB 61 GVPARFSGSGSGTDFLTNIHPVEEEDATYYCOHSRELPLTFGAGTKLELK 111

RESULT 8
 KV3T_MOUSE STANDARD; PRT; 111 AA.

P01672;
 21-JUL-1986 (rel. 01, Created)
 21-JUL-1986 (rel. 01, Last sequence update)
 15-JUL-1999 (rel. 38, Last annotation update)
 19 kappa chain V-III region PC 7940.
 DE Ig kappa chain V-III region PC 7940.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: C01938; KYMS40.
 DR HSSP: P80362; IWTL.
 DR InterPro: IPR007110; Ig_1like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.

FRAMWORK-1.
 COMPLEMENTARITY-DETERMINING-1.
 FRAMWORK-2.
 COMPLEMENTARITY-DETERMINING-2.
 FRAMWORK-3.
 COMPLEMENTARITY-DETERMINING-3.
 FRAMWORK-4.
 BY SIMILARITY.
 SEQUENCE 111 AA; 12038 MW; EE8A82306084352E CRC64;

Query Match 80.8%; Score 470.5; DB 1; Length 111;
 Best Local Similarity 83.8%; Pred. No. 3.4e-40;
 Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASQSYVDGDSYM-WYQKPGQPKLLTYAASNLSS 59
 DB 1 DIVLTQSPASLAVSLGQRATISCKRASKSVSTSGYSYMHMYQKPGQPKLLTYLASNLSS 60
 QY 60 GIPARFSGSGSGTDFLTNIHPVEEEDATYYCOLCNEPPTGAGTKLELK 110
 DB 61 GVPARFSGSGSGTDFLTNIHPVEEEDATYYCOHSRELPLTFGAGTKLELK 111

RESULT 9
 KV3R_MOUSE STANDARD; PRT; 111 AA.
 ID KV3R_MOUSE
 AC P01670;

DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 6684.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01938; KYMS84.
 DR HSSP: P80362; IWTL.
 DR InterPro: IPR007110; Ig_1like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.

FRAMWORK-1.
 COMPLEMENTARITY-DETERMINING-1.
 FRAMWORK-2.
 COMPLEMENTARITY-DETERMINING-2.
 FRAMWORK-3.
 COMPLEMENTARITY-DETERMINING-3.
 FRAMWORK-4.
 BY SIMILARITY.
 SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 80.5%; Score 468.5; DB 1; Length 111;
 Best Local Similarity 83.8%; Pred. No. 5.4e-40;
 Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASLAVSLGQRATISCKASQSYVDGDSYM-WYQKPGQPKLLTYAASNLSS 59
 DB 1 DIVLTQSPASLAVSLGQRATISCKRASKSVSTSGYSYMHMYQKPGQPKLLTYLASNLSS 60
 QY 60 GIPARFSGSGSGTDFLTNIHPVEEEDATYYCOLCNEPPTGAGTKLELK 110
 DB 61 GVPARFSGSGSGTDFLTNIHPVEEEDATYYCOHSRELPLTFGAGTKLELK 111

RESULT 10
 KV3H_MOUSE STANDARD; PRT; 111 AA.
 ID KV3H_MOUSE
 AC P01660;

DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 3741/TEPC 111.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (PC 3741).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01938; KYMS84.
 DR HSSP: P80362; IWTL.
 DR InterPro: IPR007110; Ig_1like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.

FRAMWORK-1.
 COMPLEMENTARITY-DETERMINING-1.
 FRAMWORK-2.
 COMPLEMENTARITY-DETERMINING-2.
 FRAMWORK-3.
 COMPLEMENTARITY-DETERMINING-3.
 FRAMWORK-4.
 BY SIMILARITY.
 SEQUENCE (TEPC 111).
 MEDLINE=79012520; PubMed=99744;
 McKean D.J., Bell M., Potter M.;
 "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";

RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -1- MISCELLANEOUS: THE PC 3741 AND TERC 111 SEQUENCES ARE IDENTICAL.
 DR PIR: A93204; KYMS37.
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 111 FRAMEWORK-4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 78.3%; Score 455.5; DB 1; Length 111;
 Best Local Similarity 81.1%; Pred. No. 1.1e-38;
 Matches 90; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 59
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 60
 QY 60 GIPARFSGSGGTDFLTNIHPVEEDAAATYQCLNEDPPTGAGTKLEK 110
 DB 61 GIPARFSGSGGTDFLTNIHPVEADDAATYQCOQNNEDPPTGAGTKLEK 111

RESULT 11
 KVK_MOUSE
 ID KVK_MOUSE STANDARD; PRT; 111 AA.
 AC P01663;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 4050.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_Taxid=10090;
 (1)
 SEQUENCE:
 MEDLINE-79073152; PubMed-103003;
 Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;
 RT *Rearrangement of genetic information may produce immunoglobulin
 RT diversity.*
 RL Nature 276:785-790(1978).
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 111 FRAMEWORK-4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SEQUENCE 111 AA; 12005 MW; 39DB7619313453CB CRC64;

Query Match 78.3%; Score 455.5; DB 1; Length 111;
 Best Local Similarity 82.0%; Pred. No. 1.1e-38;
 Matches 91; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 59
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 60
 QY 60 GIPARFSGSGGTDFLTNIHPVEEDAAATYQCLNEDPPTGAGTKLEK 110
 DB 61 GIPARFSGSGGTDFLTNIHPVEADDAATYQCOQNNEDPPTGAGTKLEK 111

RESULT 12
 KVK_MOUSE
 ID KVK_MOUSE STANDARD; PRT; 111 AA.
 AC P01673;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 2485/PC 4039.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_Taxid=10090;
 (1)
 SEQUENCE:
 MEDLINE-79073152; PubMed-103003;
 Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;
 RT *Rearrangement of genetic information may produce immunoglobulin
 RT diversity.*
 RL Nature 276:785-790(1978).
 CC -1- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
 DR PIR: A01939; KYMS85.
 DR HSSP: P01679; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 111 FRAMEWORK-4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SEQUENCE 111 AA; 11986 MW; BF38C59AA7858467 CRC64;

Query Match 78.1%; Score 454.5; DB 1; Length 111;
 Best Local Similarity 82.9%; Pred. No. 1.3e-38;
 Matches 92; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 59
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPKLLTYAASNL5 60
 QY 60 GIPARFSGSGGTDFLTNIHPVEEDAAATYQCLNEDPPTGAGTKLEK 110
 DB 61 GIPARFSGSGGTDFLTNIHPVEADDAATYQCOQNNEDPPTGAGTKLEK 111

RESULT 13
 KVK_MOUSE
 ID KVK_MOUSE STANDARD; PRT; 111 AA.
 AC P01662;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=99744;
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP MEDLINE=103003;
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gathmann L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
-1 MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
HSSP: P01679; 2FRJ.
InterPro: IPR007110; IG-like.
InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; Ig; 1.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;
Query Match 77.2%; Score 449.5; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 4,2e-38;
Matches 89; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
QY 1 DIVLTNSPASLAVSLGQRTATSCAKSQSDVDGDSYM-WYQKPGQPKLLTYAASNLS 59
DB 1 NIVLTQSPASLAVSLGQRTATSCRAESVDYGSFMMWYQKPGQPKLLTYLASNLS 60
60 GIPARFSSGSGTDFLTINIHVEEDATYYCOLCNEDEPPTFGAGTKLEK 110
61 GVPARFSSGSGRTDFTLTIDPEADATYYCQQNNEDPPTFGGKTLEIK 111
RESULT 14
KV3C_MOUSE STANDARD; PRT; 131 AA.
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=99744;
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).

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RN [2]
RP MEDLINE=4691517;
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR: B90412; KVM5M6.
DR HSSP: P01679; 2FRJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match 77.1%; Score 448.5; DB 1; Length 131;
Best Local Similarity 80.2%; Pred. No. 6,4e-38;
Matches 89; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
QY 1 DIVLTNSPASLAVSLGQRTATSCAKSQSDVDGDSYM-WYQKPGQPKLLTYAASNLS 59
DB 21 NIVLTQSPASLAVSLGQRTATSCRAESVDYGSFMMWYQKPGQPKLLTYLASNLS 80
60 GIPARFSSGSGTDFLTINIHVEEDATYYCOLCNEDEPPTFGAGTKLEK 110
81 GVPARFSSGSGRTDFTLTIDPEADATYYCQQNNEDPPTFGGKTLEIK 131
RESULT 15
KV3C_MOUSE STANDARD; PRT; 111 AA.
AC P01656;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 70.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=412631;
RX MEDLINE=67056897; PubMed=412631;
RA Gray W.R., Dreyer W.J., Hood L.E.;
RT "Mechanism of antibody synthesis: size differences between mouse
RT kappa chains.";
RL Science 155:465-467(1967).
-1 MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR HSSP: P01679; 2FRJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; Ig_v.

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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:46:55 : Search time 84 Seconds

(without alignments)
337.926 Million cell updates/sec

Title: US-09-759-112a-24

Sequence: 1 DIVLTNSPASPASVLSGCRAT.....CQLCNEDPPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_protist:*
11: sp_rickettsia:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467.5	80.3	111	11	Q920E9 mus musculus
2	413.5	71.0	103	11	Q9JL80 mus musculus
3	352.5	60.6	108	4	Q9UL70 mus musculus
4	348.5	59.9	108	4	Q9UL79 mus musculus
5	346	59.5	109	4	Q9UL78 mus musculus
6	342	58.8	108	4	Q9UL77 mus musculus
7	341.5	58.7	108	4	Q9UL76 mus musculus
8	341.5	58.7	108	4	Q9UL75 mus musculus
9	341.5	58.6	107	4	Q9UL74 mus musculus
10	340	58.4	112	11	Q9UL73 mus musculus
11	338.5	58.2	108	4	Q9UL72 mus musculus
12	335	57.6	109	4	Q9UL71 mus musculus
13	335	57.6	112	11	Q9UL70 mus musculus
14	334	57.4	112	11	Q9UL69 mus musculus
15	334	57.4	112	11	Q9UL68 mus musculus
16	330	56.7	114	11	Q9UL67 mus musculus

17	327	56.2	239	11	Q9VCS5 mus musculus
18	325.5	55.9	114	4	Q9UL80 mus musculus
19	325	55.8	107	4	Q9UL81 mus musculus
20	324	55.7	239	4	Q9NEK0 mus musculus
21	321.5	55.2	108	11	Q9UL70 mus musculus
22	314	54.0	106	5	Q9UL40 mus musculus
23	313.5	53.9	214	11	Q9UL45 mus musculus
24	312	53.6	239	11	Q9UL46 mus musculus
25	311	53.4	109	4	Q9UL47 mus musculus
26	311	53.4	112	11	Q9UL48 mus musculus
27	309.5	53.2	107	11	Q9UL49 mus musculus
28	308	52.9	134	11	Q9UL50 mus musculus
29	306.5	52.7	234	11	Q9UL51 mus musculus
30	305.5	52.5	234	11	Q9UL52 mus musculus
31	305	52.4	104	11	Q9UL53 mus musculus
32	305	52.4	235	11	Q9UL54 mus musculus
33	304.5	52.3	218	11	Q9UL55 mus musculus
34	301.5	51.8	99	11	Q9UL56 mus musculus
35	299.5	51.5	233	11	Q9UL57 mus musculus
36	294.5	50.6	234	11	Q9UL58 mus musculus
37	293.5	50.4	298	11	Q9UL59 mus musculus
38	291.5	50.1	109	11	Q9UL60 mus musculus
39	289.5	49.7	107	11	Q9UL61 mus musculus
40	288.5	49.6	116	4	Q9UL62 mus musculus
41	288.5	49.6	234	11	Q9UL63 mus musculus
42	286.5	49.2	97	11	Q9UL64 mus musculus
43	283.5	48.7	101	11	Q9UL65 mus musculus
44	280	48.1	148	11	Q9UL66 mus musculus
45	279.5	48.0	109	6	Q9UL67 mus musculus

ALIGNMENTS

RESULT 1
ID Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;

DT 01-DEC-2001 (TREMUR, 19, Created)

DT 01-DEC-2001 (TREMUR, 19, Last sequence update)

DT 01-MAR-2003 (TREMUR, 23, Last annotation update)

DE Pterin-mimicking anti-idiotypic kappa chain variable region

DE (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Atkin J.D., Iape A., Jennings I.G., Horvath O., Cotton R.G.H.;

RT "Definition of the Idiotypic Pterin-mimicking Antibodies Expressed

in Mammalian Cells."

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF307935; AL09419.1; -

DR InterPro: IPR007110; IG-Like.

DR InterPro: IPR003006; IG-MHC.

DR InterPro: IPR003596; IG-V.

DR Pfam: PF00047; IG; 1.

DR SMART: SM00406; IG; 1.

DR PROSITE: PS00835; IG-Like; 1.

FT NON_TER 1

FT NON_TER 111

SEQUENCE 111 AA; 12046 MW; 1E46988AA685826 CRC64;

Query Match 80.3%; Score 467.5; DB 11; Length 111;

Best Local Similarity 83.8%; Pred. No. 1.5e-43;

Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASPASVLSGCRATISCKASQSVYDDSYN-WIQQRGCPKLLTAASLES 59

DB 1 DIVLTNSPASPASVLSGCRATISCKASQSVYDDSYN-WIQQRGCPKLLTAASLES 60

QY 60 GIPARFGSGSGTDFLTINHPVEEDATATYCCQLCNEDPPTFGAGTKLELK 110

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Db      61 GVPAFSSGSGCTDFTLNTHHPVEEDATATTCQHSRELPLPYTGGGTGLEIK 111
      1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 2
09JL80 ID ID PRELIMINARY: PRT: 103 AA.
09JL80
AC 09JL80:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Anti-myosin Immunoglobulin light chain variable region
   (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
NC STRAIN=BAJB/c;
MEDLINE=20448942; PubMed=10992488;
Maikiel S., Liao L., Cunningham M.W., Diamond B.;
"Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
Infect. Immun. 68:5803-5808 (2000).
RL EMBL; AF206026; AAF69324.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-1ike.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR NON_TER 1 1
FT NON_TER
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AB21 CRC64;
Query Match 71.0%; Score 413.5; DB 11; Length 103;
Best Local Similarity 77.7%; Pred. No. 1.1e-37;
Matches 80; Conservative 10; Mismatches 12; Indels 1; Gaps 1
0Y 9 ASLAVSLGQRATTSKASQSYDVDDSDYRW-WYQOKRGPGPKLLTYAASNLSEGIPARFSG 67
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ASLAVSLGQRATTSKASQSYDVDDSDYRW-WYQOKRGPGPKLLTYAASNLSEGIPARFSG 60
0Y 68 SGSGTDFTLNTHHPVEEDATATTCQHSRELPLPYTGGGTGLEIK 110
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      61 SGSGTDFSLNTHHPVEEDATATTCQHSRELPLPYTGGGTGLEIK 103
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 3
09JL70 ID ID PRELIMINARY: PRT: 108 AA.
09JL70
AC 09JL70:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Myosin-reactive Immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
NC MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
Clin. Immunol. Immunopathol. 87:184-192 (1998).
RL EMBL; AF035044; AAD56280.1; -.

```

[illegible]

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AC Q9UL78;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; AF035036; AAD56272.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 109 AA; 11646 MW; 5675C52EC7E197 CRC64;
SQ
Query Match
Best Local Similarity 59.5%; Score 346; DB 4; Length 109;
Matches 69; Conservative 14; Mismatches 24; Indels 4; Gaps 2;
OY 1 DIVLTNSPASIYSLGQATISCKASQSVYDGDGYM-WYQKPGQPKLLTYAASNLES 59
DB 1 EIVLTQSPGTLISLPGERATISCRASQSV--SSYLAWYQKPGKAPRLITYGASSRAT 57
OY 60 GIPARFSGSGGTFTLTIHVEEDATYYCQCLNEDPPTFGAGTKLEIK 110
DB 58 GIPDRFSGSGGTFTLTIHVEEDATYYCQCLNEDPPTFGAGTKLEIK 108
ID Q8VC16 PRELIMINARY; PRT; 238 AA.
OY 08VC16;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
Query Match
Best Local Similarity 58.8%; Score 342; DB 11; Length 238;
Matches 68; Conservative 14; Mismatches 28; Indels 2; Gaps 2;
```

```
OY 1 DIVLTNSPASIYSLGQATISCKASQSVYDGDGYM-WYQKPGQPKLLTYAASNLE 58
DB 20 DVWTFQTPSLPSVSLGGQASISCSQSLVNSNNTLHWLQKPGQPKLLITKYSNRF 79
OY 59 SGIPARFSGSGGTFTLTIHVEEDATYYCQCLNEDPPTFGAGTKLEIK 110
DB 80 SGVDRFSGSGGTFTLTIHVEEDATYYCQCLNEDPPTFGAGTKLEIK 131
RESULT 7
OY 09UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; AF035037; AAD56273.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
SQ
Query Match
Best Local Similarity 58.7%; Score 341.5; DB 4; Length 108;
Matches 67; Conservative 17; Mismatches 22; Indels 5; Gaps 2;
OY 1 DIVLTNSPASIYSLGQATISCKASQSVYDGDGYM-WYQKPGQPKLLTYAASNLES 59
DB 1 DIQQTSPSPSLASVSGDRVITTCRASQSI---SSYLAWYQKPGKAPRLITYGASSIQS 56
OY 60 GIPARFSGSGGTFTLTIHVEEDATYYCQCLNEDPPTFGAGTKLEIK 110
DB 57 GVPDRFSGSGGTFTLTIHVEEDATYYCQCLNEDPPTFGAGTKLEIK 107
ID Q8NEK1 PRELIMINARY; PRT; 234 AA.
OY 08NEK1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030813; AAH30813.1; -.
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DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig: 2.
 DR SMART: SM00407; IGH1.1.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Hypothetical protein.
 SO SEQUENCE 234 AA; 25530 MW; 6316BDEFD132F8 CRC64;

Query Match 58.7%; Score 341.5; DB 4; Length 234;
 Best Local Similarity 60.0%; Pred. No. 2.4e-29;
 Matches 66; Conservative 18; Mismatches 23; Indels 3; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRTATSCKASQSYVDGDSYM-WYQKPGQPKLLTYAASNLSS 60
 DB 21 EIVMTQSPATLSVSGERATLSCRASQSYT---SNLAWYQTPGQSPRLVITGASSRASG 77
 61 IPARFSGSGSGTDFTLNIHPVEEDAAATYVYCOLCNEDEPPTFGAGTKLELK 110
 78 VPARFSGSGSGTDFTLTISLQSDPAVYVYCOQYKWKPHPTFGGTRKLDIK 127

RESULT 9

ID 096SA9 PRELIMINARY; PRT; 107 AA.

AC 096SA9:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglicosamine/anti-mysin
 RT antibody V region genes.";
 RT J. Immunol. 161:2020-2031(1998).
 RL J. Immunol. 161:2020-2031(1998).
 DR EMBL: U96396; AAB68785.1; -
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig: 1.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 107
 SO SEQUENCE 107 AA; 11520 MW; 4B843E9C5B577F16 CRC64;

Query Match 58.6%; Score 341; DB 4; Length 107;
 Best Local Similarity 61.3%; Pred. No. 1e-29;
 Matches 68; Conservative 18; Mismatches 19; Indels 6; Gaps 3;

QY 1 DIVLTNSPASLAVSLGQRTATSCKASQSYVDGDSYM-WYQKPGQPKLLTYAASNLSS 59
 DB 1 DIOMTQSPATLSVSGERATLSCRASQSYT---SSYLMWYQKPGKAPRLTYAASNLSS 56
 60 GIPARFSGSGSGTDFTLNIHPVEEDAAATYVYCOLCNEDEPPTFGAGTKLELK 110
 57 GVPARFSGSGSGTDFTLTISLQSDPAVYVYCOQYKWKPHPTFGGTRKLDIK 106

RESULT 10
 ID 08K1F2 PRELIMINARY; PRT; 112 AA.

AC 08K1F2;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 DE Mus musculus (mouse).
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RT "Innate proteolytic antibodies: failed D-VIPase response to the D-
 RT entolimier of VIP and identification of L-VIPase VL domains.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF516283; AAM64201.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig: 1.
 DR SMART: SM00409; IG: 1.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 112
 SO SEQUENCE 112 AA; 11953 MW; 4716B87FAD8543ED CRC64;

Query Match 58.4%; Score 340; DB 11; Length 112;
 Best Local Similarity 63.1%; Pred. No. 1.4e-29;
 Matches 70; Conservative 12; Mismatches 23; Indels 6; Gaps 2;

QY 1 DIVLTNSPASLAVSLGQRTATSCKASQSYVDGDSYM-WYQKPGQPKLLTYAASNLSS 59
 DB 1 DIVLTQSPATLSVSGERATLSCRASQSYT---SYMHWYQKPGKAPRLTYAASNLSS 55
 60 GIPARFSGSGSGTDFTLNIHPVEEDAAATYVYCOLCNEDEPPTFGAGTKLELK 110
 56 GVPARFSGSGSGTDFTLTISLQSDPAVYVYCOQYKWKPHPTFGGTRKLDIK 106

RESULT 11
 ID 09UL83 PRELIMINARY; PRT; 108 AA.

AC 09UL83:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetuses.";
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 RL EMBL: AF035031; AAD56267.1; -
 DR HSP: P80362; 1WTL.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig: 1.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 108

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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:55:26 ; Search time 54 Seconds
(without alignments)
297.229 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582
Sequence: 1 DIVLNSPASTAVSLGQRAT.....COLCNDPPTFGAGTKLELK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 541936
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications -AA: *
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: *
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep: *
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep: *
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep: *
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep: *
16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep: *
17: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep: *
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	110	11	US-09-759-112a-24
2	537.5	92.4	132	10	US-09-879-461-2
3	528.5	90.8	238	15	US-10-216-484-11
4	526.5	90.5	238	10	US-09-903-327A-4
5	505.5	86.9	112	15	US-10-194-975-115
6	503.5	86.5	106	9	US-09-802-077-6
7	503.5	86.5	106	9	US-09-802-096-6
8	503.5	86.5	106	11	US-09-925-179-6
9	491.5	84.5	111	9	US-09-802-077-2
10	491.5	84.5	111	9	US-09-802-096-2
11	491.5	84.5	111	11	US-09-925-179-2
12	490	84.2	112	12	US-10-160-506-81
13	487.5	83.8	238	15	US-10-216-484-34
14	485.5	83.4	111	9	US-09-920-171-5
15	485.5	83.4	111	12	US-10-113-996-5

16	476.5	81.9	238	15	US-10-216-484-52	Sequence 52, Appl
17	475.5	81.7	238	15	US-10-216-484-109	Sequence 109, App
18	475.5	81.7	271	12	US-10-053-590-12	Sequence 12, Appl
19	473.5	81.7	271	15	US-10-207-655-12	Sequence 12, Appl
20	469.5	80.7	131	10	US-09-879-461-58	Sequence 58, Appl
21	463.5	79.6	131	10	US-09-879-461-14	Sequence 14, Appl
22	461.5	79.3	112	9	US-09-810-502-37	Sequence 37, Appl
23	459.5	79.0	112	9	US-09-144-886-80	Sequence 80, Appl
24	453.5	77.9	218	15	US-10-171-452A-39	Sequence 39, Appl
25	453.5	77.9	218	15	US-10-171-452A-45	Sequence 45, Appl
26	453.5	77.9	218	15	US-10-171-452A-51	Sequence 51, Appl
27	453.5	77.9	218	15	US-10-171-452A-57	Sequence 57, Appl
28	453.5	77.9	238	15	US-10-171-452A-38	Sequence 38, Appl
29	453.5	77.9	238	15	US-10-171-452A-44	Sequence 44, Appl
30	453.5	77.9	238	15	US-10-171-452A-50	Sequence 50, Appl
31	453.5	77.9	238	15	US-10-171-452A-56	Sequence 56, Appl
32	451	77.5	112	12	US-10-160-506-82	Sequence 82, Appl
33	450.5	77.4	112	10	US-09-144-886-87	Sequence 87, Appl
34	448.5	77.1	112	10	US-09-144-886-84	Sequence 84, Appl
35	448.5	77.1	129	9	US-09-839-447A-2	Sequence 2, Appl
36	448.5	77.1	129	15	US-10-153-271-2	Sequence 2, Appl
37	446.5	76.7	238	15	US-10-216-484-129	Sequence 129, App
38	444.5	76.4	112	10	US-09-144-886-85	Sequence 85, Appl
39	444	76.3	110	10	US-09-974-052-13	Sequence 13, Appl
40	444	76.3	110	10	US-09-974-051-13	Sequence 13, Appl
41	444	76.3	110	11	US-09-974-516-13	Sequence 13, Appl
42	443.5	76.2	112	10	US-09-144-886-81	Sequence 81, Appl
43	443.5	76.2	134	9	US-09-881-823-2	Sequence 2, Appl
44	443.5	76.2	238	15	US-10-216-484-131	Sequence 131, App
45	442.5	76.0	112	10	US-09-144-886-86	Sequence 86, Appl

ALIGNMENTS

US-09-759-112a-24	US-09-759-112a-24
Sequence 24, Application US/09759112A	
Publication No. US20030100741A1	
GENERAL INFORMATION:	
APPLICANT: Mueller, Sybille	
APPLICANT: Kohler, Heinz	
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LI	
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1E7, AN ANTI-IDIOTYPIC ANTIBODY REACTI	
TITLE OF INVENTION: ANTIBODIES	
FILE REFERENCE: 200-013	
CURRENT APPLICATION NUMBER: US/09/759, 112A	
CURRENT FILING DATE: 2001-01-11	
NUMBER OF SEQ ID NOS: 38	
SOFTWARE: PatentIn version 3.0	
SEQ ID NO 24	
LENGTH: 110	
TYPE: PRT	
ORGANISM: mouse	
US-09-759-112a-24	
Query Match	100.0%; Score 582; DB 11; Length 110;
Best Local Similarity	100.0%; Pred. No. 1.8e-49;
Matches 110; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 DIVLNSPASTAVSLGQRATISCKASQSDYGDSDSYMYQKPGOPKLLTYAASNLSESG 60
DB	1 DIVLNSPASTAVSLGQRATISCKASQSDYGDSDSYMYQKPGOPKLLTYAASNLSESG 60
QY	61 IPARSGSGSGTDFLTNIHPVEEDAAATYCCOLCNDPPTFGAGTKLELK 110
DB	61 IPARSGSGSGTDFLTNIHPVEEDAAATYCCOLCNDPPTFGAGTKLELK 110
RESULT 2	
US-09-879-461-2	
Sequence 2, Application US/09879461	
Publication No. US20020193575A1	

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: GENERAL INFORMATION:
: APPLICANT: Holmes, Stephen D.
: Gross, Mitchell S.
: Sylvester, Daniel R.
: TITLE OF INVENTION: Recombinant IL4 Antibodies useful in
: Treatment of IL4 Mediated Disorders
: NUMBER OF SEQUENCES: 58
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: Corporate Intellectual Property, UW2220 - 709
: Swedeland Rd.
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-2799
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/879,461
: FILING DATE: 12-Jun-2001
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/612,929
: FILING DATE: <unknown>
: APPLICATION NUMBER: US 08/136,783
: FILING DATE: 14-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Sutton, Jeffrey A.
: REGISTRATION NUMBER: 34,028
: REFERENCE/DOCKET NUMBER: P50186-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 270-5024
: TELEFAX: (215) 270-5090
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 132 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
:
: US-09-879-461-2
:
: Query Match 92.4%: Score 537.5; DB 10; Length 132;
: Best Local Similarity 93.7%: Pred. No. 4,7e-45;
: Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
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: 1 DIVLTNSPASLAVSLGQRTATISCKASQSDVDGDSYM-WYQKPGQPKLLTYASNLES 59
: |||||
: 21 DIVLTQSPASLAVSLGQRTATISCKASQSDVDGDSYMWYQKPGQPKLLTYASNLES 80
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: Oy 60 GIPARFSGSGSGTFTLNINHPVEEDDATYTCQLCNEPPTFGAGTKLEK 110
: |||||
: Db 81 GIPARFSGSGSGTFTLNINHPVEEDDATYTCQSDNEPPTFGGQTKLEIK 131
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: RESULT 3
: US-10-216-484-11
: Sequence 11, Application US/10216484
: Publication NO. US20030103976A1
: GENERAL INFORMATION:
: APPLICANT: Serizawa, No. US20030103976A1ufusa
: APPLICANT: Haruyama, Hideyuki
: APPLICANT: Nakahara, Kaori
: APPLICANT: Tamaki, Ikuko
: APPLICANT: Takahashi, Tohru
: TITLE OF INVENTION: Anti-Fas Antibodies
: FILE REFERENCE: 980126CIP/HG
: CURRENT APPLICATION NUMBER: US/10/216,484
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: US/09/499,662

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: PRIOR FILING DATE: 2000-02-09
: PRIOR APPLICATION NUMBER: US 09/053,583
: PRIOR FILING DATE: 1998-04-01
: NUMBER OF SEQ ID NOS: 165
: SEQ ID NO 11
: LENGTH: 238
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-216-484-11

Query Match
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Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

OY 1 DIVTNSPASLAWSLGORATISCKASOSVDYDGSYM-WTQQRKGQPPKLLITYAASULES 59
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DB 21 DIVTQSPASLAWSLGORATISCKASOSVDYDGSYMNWYQQRKGQPPKLLITYAASULES 80
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OY 60 GIPARFSGSGGTDFTLNHPVEEEDATATYCCNCNDPPTFGAGTLEIK 110
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DB 81 GIPARFSGSGGTDFTLNHPVEEEDATATYCCQNTNEDPMTFGGCTLEIK 131

RESULT 4
US-10-194-975-115
: Sequence 4, Application US/09903327A
: Patent No. US2002016433A1
: GENERAL INFORMATION:
: APPLICANT: Nemerow, Glen R.
: APPLICANT: Li, Eryang
: TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAA
: TITLE OF INVENTION: GENE
: FILE REFERENCE: 22908-1228
: CURRENT APPLICATION NUMBER: US/09/903,327A
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: 09/613,017
: PRIOR FILING DATE: 2000-07-10
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 238
: TYPE: PRT
: ORGANISM: Mouse
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: (0)...(0)
: OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match
Best Local Similarity 92.8%; Score 526.5; DB 10; Length 238;
Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

OY 1 DIVTNSPASLAWSLGORATISCKASOSVDYDGSYM-WTQQRKGQPPKLLITYAASULES 59
    |||||
DB 21 DIVTQSPASLAWSLGORATISCKASOSVDYDGSYMNWYQQRKGQPPKLLITYAASULES 80
    |||||

OY 60 GIPARFSGSGGTDFTLNHPVEEEDATATYCCNCNDPPTFGAGTLEIK 110
    |||||
DB 81 GIPARFSGSGGTDFTLNHPVEEEDATATYCCQNTNEDPMTFGGCTLEIK 131

RESULT 5
US-10-194-975-115
: Sequence 115, Application US/10194975
: Publication No. US20030039649A1
: GENERAL INFORMATION:
: APPLICANT: Foote, Jefferson
: TITLE OF INVENTION: Super Humanized Antibodies
: FILE REFERENCE: 501231 01
: CURRENT APPLICATION NUMBER: US/10/194,975
: CURRENT FILING DATE: 2002-10-10

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;; PRIOR APPLICATION NUMBER: US 60/305,111
;; PRIOR FILING DATE: 2001-07-12
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 115
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-10-194-975-115

Query Match 86.5%; Score 505.5; DB 15; Length 112;
Best Local Similarity 88.3%; Pred. No. 5.2e-42;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSLGKATISCKASQSVYDGDGYM-WYQKRGKGPPLKLTYYAASNLES 59
Db 1 DIVLTQSPASLAVSLGKATISCKASQSVYDGDGYM-WYQKRGKGPPLKLTYYAASNLES 60

60 GIPARFSGSGSGTDFLTINIHVPEEEDATATYCCQNSNEDPPTFGAGT 110
61 GIPARFSGSGSGTDFLTINIHVPEEEDATATYCCQNSNEDPPTFGAGT 111

RESULT 6
US-09-802-077-6
;; Sequence 6, Application US/09802077
;; Patent No. US20010033842A1
;; GENERAL INFORMATION:
;; APPLICANT: Jardieu, Paula M.
;; APPLICANT: Presta, Leonard G.
;; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
;; FILE REFERENCE: P0718P2C3US
;; CURRENT APPLICATION NUMBER: US/09/802,077
;; CURRENT FILING DATE: 2001-03-08
;; PRIOR APPLICATION NUMBER: US 08/405,617
;; PRIOR FILING DATE: 1995-03-15
;; PRIOR APPLICATION NUMBER: US 08/185,899
;; PRIOR FILING DATE: 1994-01-26
;; PRIOR APPLICATION NUMBER: PCT/US92/06860
;; PRIOR FILING DATE: 1992-08-14
;; PRIOR APPLICATION NUMBER: US 07/879,495
;; PRIOR FILING DATE: 1992-05-07
;; PRIOR APPLICATION NUMBER: US 07/744,768
;; PRIOR FILING DATE: 1991-08-14
;; NUMBER OF SEQ ID NOS: 64
;; SEQ ID NO 6
;; LENGTH: 106
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-802-077-6

Query Match 86.5%; Score 503.5; DB 9; Length 106;
Best Local Similarity 93.4%; Pred. No. 7.6e-42;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSLGKATISCKASQSVYDGDGYM-WYQKRGKGPPLKLTYYAASNLES 59
Db 1 DIVLTQSPASLAVSLGKATISCKASQSVYDGDGYM-WYQKRGKGPPLKLTYYAASNLES 60

QY 60 GIPARFSGSGSGTDFLTINIHVPEEEDATATYCCQNSNEDPPTFGAGT 105
Db 61 GIPARFSGSGSGTDFLTINIHVPEEEDATATYCCQNSNEDPPTFGAGT 106

RESULT 7
US-09-802-096-6
;; Sequence 6, Application US/09802096
;; Patent No. US20010033839A1
;; GENERAL INFORMATION:
;; APPLICANT: Jardieu, Paula M.
;; APPLICANT: Presta, Leonard G.
;; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
;; FILE REFERENCE: P0718P2C3US

;; CURRENT APPLICATION NUMBER: US/09/802,096
;; CURRENT FILING DATE: 2001-03-08
;; PRIOR APPLICATION NUMBER: US 08/405,617
;; PRIOR FILING DATE: 1995-03-15
;; PRIOR APPLICATION NUMBER: US 08/185,899
;; PRIOR FILING DATE: 1994-01-26
;; PRIOR APPLICATION NUMBER: PCT/US92/06860
;; PRIOR FILING DATE: 1992-08-14
;; PRIOR APPLICATION NUMBER: US 07/879,495
;; PRIOR FILING DATE: 1992-05-07
;; PRIOR APPLICATION NUMBER: US 07/744,768
;; PRIOR FILING DATE: 1991-08-14
;; NUMBER OF SEQ ID NOS: 64
;; SEQ ID NO 6
;; LENGTH: 106
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-802-096-6

Query Match 86.5%; Score 503.5; DB 9; Length 106;
Best Local Similarity 93.4%; Pred. No. 7.6e-42;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSLGKATISCKASQSVYDGDGYM-WYQKRGKGPPLKLTYYAASNLES 59
Db 1 DIVLTQSPASLAVSLGKATISCKASQSVYDGDGYM-WYQKRGKGPPLKLTYYAASNLES 60

QY 60 GIPARFSGSGSGTDFLTINIHVPEEEDATATYCCQNSNEDPPTFGAGT 105
Db 61 GIPARFSGSGSGTDFLTINIHVPEEEDATATYCCQNSNEDPPTFGAGT 106

RESULT 8
US-09-925-179-6
;; Sequence 6, Application US/09925179
;; Publication No. US20030044858A1
;; GENERAL INFORMATION:
;; APPLICANT: Jardieu, Paula M.
;; APPLICANT: Presta, Leonard G.
;; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
;; FILE REFERENCE: P0718P2C3US
;; CURRENT APPLICATION NUMBER: US/09/925,179
;; CURRENT FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 08/466,163
;; PRIOR FILING DATE: 1995-06-06
;; PRIOR APPLICATION NUMBER: US 08/405,617
;; PRIOR FILING DATE: 1995-03-15
;; PRIOR APPLICATION NUMBER: US 08/185,899
;; PRIOR FILING DATE: 1994-01-26
;; PRIOR APPLICATION NUMBER: PCT/US92/06860
;; PRIOR FILING DATE: 1992-08-14
;; PRIOR APPLICATION NUMBER: US 07/879,495
;; PRIOR FILING DATE: 1992-05-07
;; PRIOR APPLICATION NUMBER: US 07/744,768
;; PRIOR FILING DATE: 1991-08-14
;; NUMBER OF SEQ ID NOS: 68
;; SEQ ID NO 6
;; LENGTH: 106
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-925-179-6

Query Match 86.5%; Score 503.5; DB 11; Length 106;
Best Local Similarity 93.4%; Pred. No. 7.6e-42;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASTAVSLGKATISCKASQSVYDGDGYM-WYQKRGKGPPLKLTYYAASNLES 59
Db 1 DIVLTQSPASLAVSLGKATISCKASQSVYDGDGYM-WYQKRGKGPPLKLTYYAASNLES 60

QY 60 GIPARFSGSGSGTDFLTINIHVPEEEDATATYCCQNSNEDPPTFGAGT 105
Db 61 GIPARFSGSGSGTDFLTINIHVPEEEDATATYCCQNSNEDPPTFGAGT 106

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RESULT 9
US-09-802-077-2
; Sequence 2, Application US/09802077
; Patent No. US2001003842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-2

Query Match      84.5%: Score 491.5; DB 9; Length 111;
Best Local Similarity 88.3%: Pred. No. 1.2e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

OY 1 DIVLTNSPASTSLAVSGORATISCKASQSYVDGDSYM-WYQOKPCQPPKLLTYAASNLSS 59
DB 1 DIVLTQSPASTSLAVSLGQRTATISCKASQSYVDGDSYMMNYQOKPCQPPKLLTYAASYLGS 60
OY 60 GIPARFSGSGCTDFTLNINHIVEEDAAATYYCQLCNEDPPTFGAGTKLELK 110
DB 61 EIPARFSGSGCTDFTLNINHIVEEDAAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 10
US-09-802-096-2
; Sequence 2, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-2

Query Match      84.5%: Score 491.5; DB 9; Length 111;
Best Local Similarity 88.3%: Pred. No. 1.2e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;
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Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

OY 1 DIVLTNSPASTSLAVSGORATISCKASQSYVDGDSYM-WYQOKPCQPPKLLTYAASNLSS 59
DB 1 DIVLTQSPASTSLAVSLGQRTATISCKASQSYVDGDSYMMNYQOKPCQPPKLLTYAASYLGS 60
OY 60 GIPARFSGSGCTDFTLNINHIVEEDAAATYYCQLCNEDPPTFGAGTKLELK 110
DB 61 EIPARFSGSGCTDFTLNINHIVEEDAAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 11
US-09-925-179-2
; Sequence 2, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C3US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-2

Query Match      84.5%: Score 491.5; DB 11; Length 111;
Best Local Similarity 88.3%: Pred. No. 1.2e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

OY 1 DIVLTNSPASTSLAVSGORATISCKASQSYVDGDSYM-WYQOKPCQPPKLLTYAASNLSS 59
DB 1 DIVLTQSPASTSLAVSLGQRTATISCKASQSYVDGDSYMMNYQOKPCQPPKLLTYAASYLGS 60
OY 60 GIPARFSGSGCTDFTLNINHIVEEDAAATYYCQLCNEDPPTFGAGTKLELK 110
DB 61 EIPARFSGSGCTDFTLNINHIVEEDAAATFYCQSHEDPYTFGAGTKLEIK 111

RESULT 12
US-10-160-506-81
; Sequence 81, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; FILE REFERENCE: 10448-162001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
```


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anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antifertility; neuroprotective; antiartherosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.

Mus musculus.

EP990663-AZ.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY) SANKYO CO LTD.

Serizawa N, Haryama H, Nakahara K, Tamaki I, Takahashi T; WPI: 2000-258930/23.

P-PSDB: AAM90898.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Example reference 4; Page 102-103; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antifertility, neuroprotective, antiartherosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (II) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, Rheumatoid arthritis, graft versus host disease, Sjogren's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence encodes a murine anti-Fas monoclonal antibody HFE7A light chain described in the method of the invention.

Sequence 714 BP: 200 A; 184 C; 173 G; 157 T; 0 other;

Query Match 88.8%; Score 293; DB 21; Length 714;

Best Local Similarity 94.6%; Pred. No. 8.5e-81;

Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

1 GACATTGGTCACCAATTCACCTCTTGGCTGTCTCTAGGCGAGGCGCAC 60
|||||
61 GACATTGGTCACCAATTCACCTCTTGGCTGTCTCTAGGCGAGGCGCAC 120

ATCTCTCGACAGCCCAAGTGTGATTTGATGGTATATG---TGTAC 117
|||||
121 ATCTCTCGACAGCCCAAGTGTGATTTGATGGTATATGAGTACTGTAC 180
118 CACAGAAACGACGAGCAGCCCAACCTCTACCTATGTCATTCATTAATCT 177
|||||
181 CACAGAAACGACGAGCAGCCCAACCTCTACCTATGTCATTCATTAATCT 240
178 GGGATCCACGACGATTTAGTGGAGTGGGTGGACAGACTTCACTCAATCCAT 237
|||||
241 GGGATCCACGACGATTTAGTGGAGTGGGTGGACAGACTTCACTCAATCCAT 300
238 CCTGTGAGAGAGAGATGCTGCAACCTATTACTGACCTTGTATGAGATCTGCC 297
|||||
301 CCTGTGAGAGAGAGATGCTGCAACCTATTACTGACCAAGATATGAGATCTCGG 360
298 ACGTTGGTGTCTGGACCAAGCTGAGCTGAAA 330
|||||
361 ACGTTGGTGTGGAGCACCAGCTGAAATCAAA 393

RESULT 11

ABL45926 standard; CDNA; 714 BP.

ABL45926;

26-APR-2002 (first entry)

Mouse humanised anti-Fas antibody related cDNA SEQ ID NO 8.

Human: mouse; humanised anti-Fas antibody; Fas/Fas ligand;

light chain subunit; apoptosis; immunosuppressive; anti-allergic;

autoimmune disease; allergy; atopic; ss.

Mus musculus.

JP2001342148-A.

11-DEC-2001.

28-MAR-2001; 2001JP-0093106.

29-MAR-2000; 2000JP-0090918.

(SANY) SANKYO CO LTD.

WPI: 2002-145113/19.

P-PSDB: ABB74904.

Drug containing humanised anti-Fas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy.

Example 4 (Preparatory): Page 77-79; 194pp; Japanese.

The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and anti-allergic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others.

Sequence 714 BP: 200 A; 184 C; 173 G; 157 T; 0 other;

Query Match 88.8%; Score 293; DB 24; Length 714;

Best Local Similarity 94.6%; Pred. No. 8.5e-81;

Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

1 GACATTGGTCACCAATTCACCTCTTGGCTGTCTCTAGGCGAGGCGCAC 60

DB 127 ATCTCTCAAGGCGCCAAAGTGTATGATGTGATAGTATATGACATGCTAC 186
QY 118 CAACGAAACGAGCAGCAGCCCAACTCCCTACCTTCGTGCATTCATTAACATCT 177
DB 187 CAACGAAACGAGCAGCAGCCCAACTCCCTACCTTCGTGCATTCATTAACATCT 246
QY 178 GGGATCCGAGCAGGTTAGTGGCAGTGGGTCTGGAGACAGCTTACCCCTCAACATCAT 237
DB 247 GGGATCCGAGCAGGTTAGTGGCAGTGGGTCTGGAGACAGCTTACCCCTCAACATCAT 306
QY 238 CCTGTGAGAGAGAGAGATGCTGCAACCTATTACTGTGAGCTTTGTAATGAGAGATCTCC 297
DB 307 CCTGTGAGAGAGAGAGATGCTGCAACCTATTACTGTGAGCTTTGTAATGAGAGATCTCC 366
QY 298 ACGTTGGTGGTGGGAGCCAGCTGAGCTGAAA 330
DB 367 ACGTTGGTGGGAGCCAGCTGGAATCAAA 399
MULT 14
AAZ58664
ID AAZ58664 standard; cDNA to mRNA; 925 BP.
AC AAZ58664;
XX
DT 17-APR-2000 (first entry)
XX
DE Antibody 4H5 L chain encoding nucleotide sequence.
XX
KW CD4 antigen; anti-human; antibody; 4H5; drug; ds.
XX
OS Mus sp.
XX
PN JP11332563-A.
XX
PD 07-DEC-1999.
XX
PF 26-MAY-1998; 98JP-0163034.
XX
PR 26-MAY-1998; 98JP-0163034.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
DR WPI: 2000-091351/08.
XX
P-PSDB: AAY59265.
XX
An antibody and the nucleic acid coding the antibody -
XX
PS Disclosure; Page 17-18; 25pp; Japanese.
XX
CC The invention provides an antibody having affinity to CD4 antigen. The
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
CC application for drugs. It is highly safe in human dose. The present
CC sequence represents the antibody 4H5 L chain encoding nucleotide
CC sequence.
SQ Sequence 925 BP; 223 A; 236 C; 268 G; 198 T; 0 other;
Query Match 88.8%; Score 293; DB 21; Length 925;
Best Local Similarity 94.6%; Pred. No. 9.3e-81;
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

DB 586 CAACGAAACGAGCAGCAGCCCAACTCCCTCATCTATGCTGATCCAACTTACATCT 645
QY 178 GGGATCCGAGCAGGTTAGTGGCAGTGGGTCTGGAGACAGCTTACCCCTCAACATCAT 237
DB 646 GGGATCCGAGCAGGTTAGTGGCAGTGGGTCTGGAGACAGCTTACCCCTCAACATCAT 705
QY 238 CCTGTGAGAGAGAGATGCTGCAACCTATTACTGTGAGCTTTGTAATGAGAGATCTCC 297
DB 706 CCTGTGAGAGAGAGATGCTGCAACCTATTACTGTGAGCTTTGTAATGAGAGATCTCC 765
QY 298 ACGTTGGTGGTGGGAGCCAGCTGAGCTGAAA 330
DB 766 ACGTTGGTGGGAGCCAGCTGGAATCAAA 798
RESULT 15
AAZ44205
ID AAZ44205 standard; DNA; 925 BP.
AC AAZ44205;
XX
DT 31-MAR-2000 (first entry)
XX
DE Murine derived DNA fragment #3.
XX
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine; ds.
XX
OS Mus sp.
XX
PN WO961629-A1.
XX
PD 02-DEC-1999.
XX
PF 24-MAY-1999; 99WO-JP02711.
XX
PR 25-MAY-1998; 98JP-0159957.
XX
PR 26-MAY-1998; 98JP-0163023.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
PA (ASAH) ASAH MEDICAL CO LTD.
XX
PI Ono M, Soka T, Morimoto I, Miyamura K.
XX
XX WPI: 2000-086720/07.
XX
DR P-PSDB: AAY51141.
XX
PT Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells -
XX
PS Claim 22; Page 80-82; 11pp; Japanese.
XX
CC This invention describes a novel device (I) for separating cluster
CC differentiation (CD)-positive cells using a recombinant (chimeric or
CC single-chain) antibody recognising CD4 or CD34. The devices are useful
CC for the separation of CD4 or CD34 positive cells, which is useful for
CC the collection of hematopoietic undifferentiated cells, elimination of
CC lymphocytes from cells to be used in bone marrow transplantation, the
CC detection of leukemic cells and the production of medicinal
CC compositions for the treatment of HIV infection and autoimmune diseases.
CC This sequence encodes a murine derived protein fragment which is used
CC to illustrate the method of the invention.
SQ Sequence 925 BP; 223 A; 236 C; 268 G; 198 T; 0 other;
Query Match 88.8%; Score 293; DB 21; Length 925;
Best Local Similarity 94.6%; Pred. No. 9.3e-81;
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 05:05:14 : Search time 2595 Seconds
(without alignments)
3090.743 Million cell updates/sec

Title: US-09-759-112a-23

Sequence: 1 gacatgtgtcaccacatc.....ggaccaagctgagctgaaa 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estda:
2: em_esthum:
3: em_estln:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hlc:
9: gb_estl:
10: gb_est2:
11: gb_hlc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_hlv:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_man:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rod:
26: em_gss_phg:
27: em_gss_vrl:
28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	250.4	75.9	659	10 BF137298 601781658
2	249.8	75.7	407	10 AW988429 u908607.y
3	245	74.2	683	11 AF240172 Mus muscu
4	245	74.2	1108	12 BG969221 602835202

5	244.8	74.2	774	10 BF581989	BF581989 602099444
6	244	73.9	73.9	12 BG965050	BG965050 602829112
7	241.8	73.3	398	10 AA423447	AA423447 v680a03.r
8	241.8	73.3	633	14 BY733441	BY733441 BY733441
9	240.4	72.8	831	12 BG966589	BG966589 602834422
10	239.6	72.6	402	9 A1549800	A1549800 v680a03.y
11	239.2	72.5	327	10 BG148320	BG148320 uu91c06.y
12	239.2	72.5	876	12 B1107286	B1107286 602894285
13	238.6	72.3	735	12 BG967206	BG967206 602833889
14	238.6	72.3	865	12 B1659552	B1659552 60303102
15	238	72.1	420	9 A1120005	A1120005 uc25e04.r
16	237.6	72.0	732	12 BG962768	BG962768 602830291
17	235.4	71.3	806	12 B1108506	B1108506 602894952
18	232.2	70.4	1063	10 BF577971	BF577971 602091801
19	224.2	67.9	922	10 BF584560	BF584560 602098269
20	216	65.5	974	10 BF577946	BF577946 602091968
21	207	62.7	286	10 BG144775	BG144775 uc77f11.y
22	201.6	61.1	339	9 AA710249	AA710249 vt49e01.r
23	200.4	60.7	266	10 BG145361	BG145361 uu71a06.y
24	199.4	60.4	344	13 BY214260	BY214260 BY214260
25	198.6	60.2	577	28 A2942606	A2942606 2M0202N14
26	175.4	53.2	671	11 AF240168	AF240168 Mus muscu
27	174.2	52.8	268	10 BG148476	BG148476 uu79a08.y
28	171.2	51.9	756	28 BH054133	BH054133 RPCI-24-3
29	169.8	51.5	757	10 BG484518	BG484518 602505173
30	164.4	49.8	465	9 AA404697	AA404697 UT-HF-BLO
31	164.4	49.8	727	14 CB956193	CB956193 AGENCOURT
32	163.8	49.6	798	10 BG426036	BG426036 602452715
33	162.2	49.2	776	14 CB959429	CB959429 AGENCOURT
34	161.2	48.8	34	12 CB957520	CB957520 AGENCOURT
35	160.6	48.7	533	9 AM802126	AM802126 IL5-UM007
36	160.6	48.7	717	14 CB957784	CB957784 AGENCOURT
37	160.6	48.7	777	14 CB957974	CB957974 AGENCOURT
38	160.6	48.7	779	14 CB986877	CB986877 AGENCOURT
39	160.6	48.7	795	14 CB986276	CB986276 AGENCOURT
40	160.6	48.7	889	14 CB985667	CB985667 AGENCOURT
41	160.4	48.6	434	9 AA406486	AA406486 UT-HF-BLO
42	160.2	48.5	808	14 CB984840	CB984840 AGENCOURT
43	159.6	48.4	482	9 AV733856	AV733856 AV733856
44	159.6	48.4	519	9 AA405183	AA405183 UT-HF-BLO
45	159.6	48.4	744	14 CB956406	CB956406 AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS BF137298
DEFINITION 601781658F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009670 5', mRNA sequence.
ACCESSION BF137298
VERSION BF137298.1 GI:10976338
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Plate: L1AM9246 row: c column: 15
High quality sequence stop: 657.

FEATURES		Location/Qualifiers
source		1..659 /organism="Mus musculus" /mol_type="mRNA" /strain="C2CH IR" /db_xref="taxon:10090" /clone="IMAGE:400670" /tissue_type="tumor, metastatic to mammary" /lab_host="DH10B" /clone_1lib="NCI-CGAP_Lu30" /note="Organ: Lung; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: SalI; transgenic model MN-1, expression driven by MMTV-ltr enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT	177 a 177 c 157 g 148 t	
ORIGIN		
Query Match	75.9%; Score 250.4; DB 10; Length 659;	
Best Local Similarity	89.3%; Pred. No. 2e-63;	
Matches	293; Conservative 0; Mismatches 31; Indels 4; Gaps 2;	
Df		
Oy	6 TGTGTCACCAATCTCCAGCTTCTTGTCGTGTCCTTAGGGCAGAGGCACCACATTC 65	
Df	42 TGTGTCACCAATCTTCAGCTTC-TTGGCTGTGTCCTTAGGGCAGAGGCACCACATTT 100	
Oy	66 CTGCAGGCCAGCCAAAGTGTGATTATGATGTGATAGTAATATG--TGGTACCAACA 122	
Df	101 CTGCAGACCAGCCAGATGCTCTATTATAATGAATAGTATATGACTGTTCACACA 160	
Oy	123 GAACACAGACAGCACCCAAATCTCTACTATGTCTCATTCATCAATCTAGAATCTGGAT 182	
Df	161 GAACACAGACAGCACCCAAATCTCTATATATGCTGCATCAACCTAAGATCTGGGGT 220	
Oy	183 CCGAACCCAGTTTACTGTGCGAGTGGGTGGGACAGACTTCACCCCTCAACATCCATCCGT 242	
Df	221 CCCTGCCAGGTTCAGTGGCAGTGGGTGGGACAGACTTCACCCCTCAACATCCATCCGT 280	
Oy	243 GGAGAGAGAGATGCTGCACACTATTACTGTCAAGCTTTTATATGATGAGATCTCCACGTT 302	
Df	281 GGAGAGAGAGATGCTGCACACTATTACTGTCAAGAGATTTATGATGATCTCCGACGTT 340	
Oy	303 CGGTCTCTGGACCAAGCTGAGCTGAAA 330	
Df	341 CGGTGAGGACCAAGCTGAAATCAA 368	
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US		
INITIATION	AW988429 407 bp mRNA linear EST 02-JUN-2000	
ACCESSION	ug08d07.y1 Soares_mammary_gland_MLNG Mus musculus cDNA clone	
VERSION	IMAGE:1531021.5' similar to gb:X02484_rnal IG KAPPA CHAIN PRECURSOR	
KEYWORDS	V-IV REGION (HUMAN); gb:M35665 Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region, (MOUSE)., mRNA sequence.	
SOURCE	AW988429 AW988429.1 GI:8183581	
ORGANISM	EST. Mus musculus (house mouse)	
JOURNAL	Mus musculus	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 407) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgepb@remail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:947121	
FEATURES	Seq primer: -40RP from Gluco. Location/Qualifiers	

[illegible]

REFERENCE	3 (bases 1 to 683)
AUTHORS	Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X. and Su,C.
TITLE	Direct Submission
JOURNAL	Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang Le West Road, Xi'an 710032, China
FEATURES	Location/Qualifiers
SOURCE	1. 683
	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="BALB/c"
	/db_xref="taxon:10090"
	/sex="male"
	/cell_type="intestinal gland cell"
	/note="derived from differential display PCR between irradiated mice with and without RNA injection"
	<1. 352
	/note="related to the repair of irradiation-damaged intestinal gland cells treated with RNA"
	/codon_start=2
	/product="MRP9"
	/protein_id="AAK3734.1"
	/db_xref="GI:13877294"
	/translation="LCGTRFORIRIRHRRCGRFQQLCPSPSRVNNLLTYEIHCRILHLHRYVEAEICPRETPASKPRDRPSLIGCSIDIEFGWLFLEPVHKNANIITNTFPGSAGDGGPLP"
BASE COUNT	153 a 199 c 167 g 163 t 1 others
ORIGIN	
Query Match	74.2%; Score 245; DB 11; Length 683;
Best Local Similarity	85.6%; Pred. No. 8e-62;
Matches	285; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
OY	1 GACATTGGCTCACCACCAATTCCTCCAGCTTCCTTGGCTGCTGCTCTAGGCGACAGGGCCACC 60
Db	
	394 GACATCGTGTCCACCCACTCTCCAGCTTCCTTGGCTGCTCTAGGCGACAGGGCCACC 335
OY	61 ATCTCTGTCAGAGGCCAGCCAAAGTGTGATTATGATGGTGAATGATATATG---TGGTAC 117
Db	
	334 ATCTCTGTCAGAGCGAGCGAAGATGTTGATATATGTCATTAATTAATGAACCTGGTTC 275
OY	118 CAACAGAAACAGACGACACGCCAACCTCTCACTATGCTGCATCCATCTAGAAATCT 177
Db	
	274 CAGCAGAAACAGACGACACGCCAACCTCTCACTATGCTGCATCCATCAACAGAAATCTC 215
	178 GGGATGCCAGCAGAGTTAGTGGGAGTGGGCTGGGACGACTCACCCTCAACATCAT 237
Db	
	214 GGGGTCCCTCGACAGTTACTTGGGAGTGGGCTGGGACGATTCACGCTCAACATATAT 155
OY	238 CCTGTGAGAGGAGAGATCTGTCAACCTATCTGATGAGCTTCTTAATGAGATCTGCC 297
Db	
	154 CCTATGAGAGGAGATGATCTGTCAACCTATCTGATGAGCTTCTTAATGAGAGATCTTAC 95
OY	298 ACCTTCGGTCTGGGACCAAGCTGAGCTGAAA 330
Db	
	94 ACCTTCGGGAGGGGAGCAACGCTGAGCTGAAA 62
RESULT 4	
LOCUS	1108 bp mRNA linear EST 12-JUN-2001
DEFINITION	602835202P1 NC1_CGAP_C024 Mus musculus cDNA clone IMAGE:4989625 5', mRNA sequence.
ACCESSION	BC969221
VERSION	BC969221.1 GI:14356858
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 1108)

AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@email.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) Clone Sequencing by: Incyte Genomics, Inc. Data Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LLM11004 row: c column: 02 High quality sequence stop: 508.	
FEATURES	Location/Qualifiers	
source	1..1108 /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4989625" /lab_host="DH10B (T1 phage-resistant)" /clone_1lb="NCI CGAP Co24" /note="Organ: colon; Vector: pCMV-Sport6; Site_1: Notf; Site_2: Salt; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP library."	
BASE COUNT	286 a 417 c 244 g 161 t	
ORIGIN		
Query Match	74.2%; Score 245; DB 12; Length 1108;	
Best Local Similarity	93.5%; Pred. No. 1.le-61;	
Matches 289; Conservative	0; Mismatches 15; Indels 5; Gaps 3;	
QY	1 GACATTGGCTCCACCATTTCACAGCTTTGTGGCTGTCTCAGGCGAGGGCCACC 60	
Dd	 63 GACTATGTGTCAGCCCACTTCACGCTTCTTGCTGTCTTAGGGCAGAGGGCCACC 122	
QY	61 ATCTCTGCGAAGGCCAGCCAAAGTGTGATTATGATGGTGTAGTATTATG--TGTAC 117	
Dd	123 ATCTCTGCGAAGGCCAGCCAAAGTGTGATTGTTGATGGTGTATATGATGAACGTGAC 182	
QY	118 CAC-AGAACCAGGACAGCACCCCAAACCTCTCACTATGCTGCATCAATCTGAAATC 176	
Dd	183 CAACCTACAACACAGACAGACGCCAACCAACTCTCATCTATCTGCATCCAATCTGAATC 242	
QY	177 TGGATCCACAGCAGGTTTATGTGCAAGGGGTCTGGGACAGACTTCACCCCAACATCCA 236	
Dd	243 TGGATACCCACAGGTTTATGTGCAAGGGGTCTGGGACAGACTTCACCCCAACATCCA 302	
QY	237 TCCTGTGAGAGAGAGAGATGCTGCAACCTATTACTGTGCAGC-TTGTGTAATGAGATCCTC 295	
Dd	303 CCCGTGTGAGAGAGAGAGATGCTGCAACCTATTACTGTGCAGCAGTAATGAGATCCTC 362	
QY	296 CCACGTTTCG 304	
Dd	363 ACACGTTTCG 371	
RESULT 5		
Bf581989	774 bp mRNA linear EST 12-DEC-2000	
LOCUS	60209944.F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219426 5',	
DEFINITION	mRNA sequence.	
ACCESSION	Bf581989	
VERSION	Bf581989.1 GI:11655610	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 774)	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .	

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

BASE COUNT	210 a	204 c	185 g	175 t
ORIGIN				

RESULT 6	
LOCUS	BC965050
DEFINITION	BC965050. 750 bp mRNA linear EST 12-JUN-2001
ACCESSION	6028291121 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4983962 5'
VERSION	BC965050
KEYWORDS	BC965050.1 GI:14352687
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 750)
	NIH-MGC http://mgc.ncl.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

BASE COUNT	202 a	193 c	181 g	174 t
ORIGIN				

RESULT 7					
AA423447					
LOCUS	AA423447	398 bp	mRNA	linear	EST 16-OCT-1997
DEFINITION	<p>veg08a03.r1 Soares_mammary_gland_NbMmC Mus musculus cDNA clone IMAGE832492 5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-IIII REGION (HUMAN); gb:M35669 Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence.</p>				
ACCESSION	AA423447				
VERSION	AA423447.1	GI:2102360			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 398)				
REFERENCE	Matra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,				
AUTHORS					

This read has been verified (found to hit its original self in the correct orientation)

Seq primer: -40RP from Gibco.

Location/Qualifiers

FEATURES

source

1.402

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:832492"

/sex="male"

/tissue_type="mammary gland"

/dev_stage="4 weeks"

/lab_host="DH10B"

/clone_lib="Soares_mammary_gland_NbMGC"

/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia)

) with a modified polylinker. Site.1: Not I; Site.2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'

TCCTACCAATCTGAAGTGGAGGCGGCCGAATGCTTTTCTTTTCTTTTCTTTT

T 3'); double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

RNA provided by Dr. Minoru Ko, Wayne State Univ. Library

constructed and normalized by Bento Soares and M. Fatima

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BASE COUNT 102 a 101 c 105 g 94 t

ORIGIN

Query Match

Best Local Similarity 72.6%; Score 239.6; DB 9; Length 402;

Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

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Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

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Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

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Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Matches 279; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

BASE COUNT 83 a 84 c 82 g 78 t

ORIGIN

Query Match

Best Local Similarity 72.5%; Score 239.2; DB 10; Length 327;

Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

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Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

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Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

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Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

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Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1088814

Seq primer: -40RP from Gibco.

Location/Qualifiers

FEATURES

source

1.327

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:3383818"

/lab_host="DH10B (phage-resistant)"

/note="Organ: germinal B-cell; Vector: pT7T3D-Pac

(Pharmacia) with a modified polylinker. Site.1: Not I;

Site.2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5'

TCCTACCAATCTGAAGTGGAGGCGGCCCTGCTTTTCTTTTCTTTTCTTTT

T 3'); double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

Library is normalized; constructed by Bento Soares and

M. Fatima Bonaldo."

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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM1108 row: 1 column: 22
High quality sequence stop: 823.
Location/Qualifiers
1..876

FEATURES
Source
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5039325"
/tissue_type="spontaneous tumor, metastatic to mammary."
/stem_cell_origin="Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: Lung; Vector: pCMV-Sport6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT
239 a 242 c 192 g 203 t
ORIGIN

Query Match 72.5%; Score 239.2; DB 12; Length 876;
Best Local Similarity 85.8%; Pred. No. 4.9e-60;
Matches 278; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

OY 10 CTCACCAATTCCTCCAGCTTCTTGCTGCTGCTCTAGGAGAGGCCACCATCTCCG 69
DB 1 CTGACCCATCTCCAGCTTCTTGCTGCTCTAGGAGAGGCCACCATCTCCG 60
OY 70 AAGGACGACCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 126
DB 61 AGAGCGATGAAAGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
OY 127 CCAGGACAGCCACCAACTCTCAGTATGCTGATGCTGATGCTGATGCTGATGCTGAT 186
DB 121 CCTGACAGCCACCAACTCTCAGTATGCTGATGCTGATGCTGATGCTGATGCTGAT 180
OY 187 GCCAGCTTACGAGGAGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
DB 181 GACAGGTTACGAGGAGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
OY 247 GAGGAGAGATGCTGCAACTATTACTGTCAGCTTTGTAATGAGAGATCTCCACGTTGCT 306
DB 241 GCTGATGATGCTGCAACTATTACTGTCAGCAAAATATGAGAGATCTCTTACGTTGGA 300
OY 307 GCTGGGACCAAGCTGGAGCTGAAA 330
DB 301 TCGGGGACCAAGCTGGAGCTGAAAATAAA 324

RESULT 13
BG967206 735 bp mRNA linear EST 12-JUN-2001
LOCUS 602833889P1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:498086 5',
DEFINITION mRNA sequence.
ACCESSION BG967206
VERSION BG967206.1 GI:14354843
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 735)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM1100 row: b column: 23
High quality sequence stop: 730.
Location/Qualifiers
1..735

FEATURES
Source
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:498086"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-Sport6; Site_1: NotI; Site_2: Salt; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library."

BASE COUNT
194 a 201 c 178 g 162 t
ORIGIN

Query Match 72.3%; Score 238.6; DB 12; Length 735;
Best Local Similarity 84.4%; Pred. No. 6.7e-60;
Matches 281; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

OY 1 GACATTTGCTCCACCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
DB 86 GACATTTGCTCCAGCACT 145
OY 61 ATCTCTCTCAAGGCCCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 117
DB 146 ATCTCTCTCAAGGCCCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 205
OY 118 CAACGAAACCAAGGACCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 177
DB 206 CAACGAAACCAAGGACCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 265
OY 178 GGGATCCAGGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 237
DB 266 GGGATCCAGGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 325
OY 238 CCTGTGAGAGAGAGATGCTGCAACTATTACTGTCAGCTTTGTAATGAGAGATCTCTCC 297
DB 326 CCTGTGAGAGAGAGATGCTGCAACTATTACTGTCAGCAAAATATGAGAGATCTCTCTCC 385
OY 298 AGCTTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 330
DB 386 AGCTTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 418

RESULT 14
B1659552 865 bp mRNA linear EST 12-SEP-2001
LOCUS 603303102P1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5340688 5',
DEFINITION mRNA sequence.
ACCESSION B1659552
VERSION B1659552.1 GI:15573788
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 865)
NIH-MGC http://mgc.nci.nih.gov/.

db 302 CCTATGAGAGAGATGATTCTGCAATGTAATTTCTGTCAGCAAAAGTAAGGAGGTTCTTTGG 361
Oy 298 ACGTTCGGTCTGGGACCAAGCTGGA 323
||||||| | | | |
db 362 ACGTTCGGTGGAGGACGAGCTGGA 387

Search completed: September 13, 2003, 06:41:26
Job time : 2602 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 05:10:03 : Search time 64 Seconds
(without alignments)
2275.882 Million cell updates/sec

Title: US-09-759-112a-23

Perfect score: 330
Sequence: 1 gacattggtcaccattc.....ggaccaagctgagctgaa 330

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

al number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294.6	89.3	396	2	US-08-483-636-1 Sequence 1, Appl
2	294.6	89.3	396	2	US-08-483-632-1 Sequence 1, Appl
3	286.6	86.8	333	1	US-08-491-845-7 Sequence 7, Appl
4	283.4	85.9	393	3	US-08-579-378A-13 Sequence 13, Appl
5	262.6	79.6	393	1	US-08-137-117D-32 Sequence 32, Appl
6	262.6	79.6	393	1	US-08-436-717-32 Sequence 32, Appl
7	261	79.1	333	1	US-08-275-053-10 Sequence 10, Appl
8	261	79.1	333	1	US-08-275-053-16 Sequence 16, Appl
9	261	79.1	363	1	US-08-111-080-21 Sequence 21, Appl
10	261	79.1	363	1	US-08-111-080-21 Sequence 21, Appl
11	261	79.1	363	5	PCT-US93-07967-21 Sequence 21, Appl
12	257.8	78.1	339	2	US-08-553-497A-9 Sequence 9, Appl
13	257.8	78.1	363	1	US-08-111-080-17 Sequence 17, Appl
14	257.8	78.1	363	5	PCT-US92-07111-16 Sequence 16, Appl
15	257.8	78.1	363	5	PCT-US93-07967-17 Sequence 17, Appl
16	257.8	78.1	363	2	US-08-553-497A-5 Sequence 5, Appl
17	254.6	77.2	393	2	US-07-634-278-66 Sequence 66, Appl
18	249.8	75.7	393	1	US-08-477-728-66 Sequence 66, Appl
19	249.8	75.7	393	1	US-08-474-040-66 Sequence 66, Appl
20	249.8	75.7	393	1	US-08-487-200-66 Sequence 66, Appl
21	249.8	75.7	393	2	US-08-621-751A-9 Sequence 9, Appl
22	249.8	75.7	393	2	US-08-484-537-66 Sequence 66, Appl
23	249.8	75.7	393	2	US-08-553-497A-17 Sequence 17, Appl
24	246.2	74.6	717	2	US-08-656-906-24 Sequence 24, Appl
25	245	74.2	906	3	US-09-217-847-24 Sequence 3, Appl
26	245	74.2	906	3	US-08-442-542-3 Sequence 3, Appl
27	243.4	73.8	333	1	US-08-483-636-1 Sequence 1, Appl

28	243.4	73.8	333	3	US-08-765-469-3 Sequence 3, Appl
29	243.4	73.8	393	1	US-08-137-117D-24 Sequence 24, Appl
30	243.4	73.8	393	1	US-08-436-717-24 Sequence 24, Appl
31	243.4	73.8	1797	1	US-08-442-542-17 Sequence 17, Appl
32	243.4	73.8	1797	3	US-08-765-469-17 Sequence 17, Appl
33	242.4	73.5	783	4	US-08-487-283A-19 Sequence 19, Appl
34	239.4	72.5	333	1	US-08-207-169A-3 Sequence 3, Appl
35	238.6	72.3	336	3	US-09-065-059-14 Sequence 14, Appl
36	237	71.8	394	4	US-08-836-561-24 Sequence 24, Appl
37	237	71.8	394	4	US-09-434-122-24 Sequence 24, Appl
38	235.4	71.3	399	5	PCT-US94-14106-52 Sequence 52, Appl
39	235.4	71.3	428	3	US-08-589-939-4 Sequence 4, Appl
40	233.8	70.8	348	2	US-08-650-262-1 Sequence 1, Appl
41	233.8	70.8	723	5	PCT-US94-14106-56 Sequence 56, Appl
42	232.2	70.4	654	5	PCT-US96-13152-1 Sequence 1, Appl
43	231.4	70.1	332	3	US-08-881-037-58 Sequence 58, Appl
44	230.6	69.9	393	3	US-08-579-378A-17 Sequence 17, Appl
45	229	69.4	396	2	US-08-379-057-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-1
Sequence 1, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sulton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

? HYPOTHETICAL: NO
 ? ANTI-SENSE: NO
 ? FRAGMENT TYPE: N-terminal
 ? ORIGINAL SOURCE:
 ? ORGANISM: mouse
 ? STRAIN: Balb/c
 ? DEVELOPMENTAL STAGE: adult
 ? TISSUE TYPE: Lymph node
 ? IMMEDIATE SOURCE:
 ? CLONE: L3 11d (light chain)
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: 1..339
 ? US-08-553-497A-9

Query Match 78.1%; Score 257.8; DB 2; Length 339;
 Best Local Similarity 88.0%; Pred. No. 1.2e-78;
 Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

1 GACATTGCTCACCACCAATTCCTCTTGGCTGTGTCTCTAGGAGAGGGCCACC 60
 1 GACATTGACCTCACCAGTCCTCAGCTTCTTGGCTGTGTCTCTAGGAGAGGGCCACC 60
 61 ATCTCTGCAAGGCCACCAAGTTGATATGATGTGATGATTATG---TGTAC 117
 61 ATCTCTGCGAGCGCCAGCAAGTGTGATTAATTTGGCATTGATTATGAACGTGTTC 120
 118 CAACAGAAACGAGAGAGAGCCCAAACTCTCACCATTGCTGATGCTCAATGATAGAT 177
 121 CACAGAAACGAGAGAGAGCCCAAACTCTCATTCTATGATGCTCAACCAAGGATCC 180
 178 GGGATCCAGCAGGTTTATGTCGAGTGGGTCTGGAGACAGCTTCAACCTCAACATCAT 237
 181 GGGGTCCCTCCAGGTTTATGTCGAGTGGGTCTGGAGACAGCTTCAACATCAT 240
 238 CCTGTGAGAGAGAGAGTCTTCAACCTTACTGTGACCTTGTATAGATGATCTCTCC 297
 241 CTTGTGAGAGAGATGATCTCAATGATTTCTGTGACCAAAATAGAGAGTCCGCTC 300
 298 ACCTTCGGTGTGGAGACCAAGCTGGAGCTGAAA 330
 301 ACCTTCGGTGTGGAGACCAAGCTGGAGCTGAAA 333

RESULT 13
 US-08-111-080-17
 ? Sequence 17, Application 08/111080
 ? Patent No. 555865
 ? GENERAL INFORMATION:

? APPLICANT: Onno, Tsuneya
 ? TITLE OF INVENTION: HIV Immunotherapeutics
 ? NUMBER OF SEQUENCES: 38
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ? STREET: 6300 Sears Tower, 233 S. Wacker Drive
 ? CITY: Chicago
 ? STATE: Illinois
 ? COUNTRY: USA
 ? ZIP: 60606
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: 08/111,080
 ? FILING DATE:
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/748,562
 ? FILING DATE: 22-AUG-1991
 ? PRIOR APPLICATION DATA:

? APPLICATION NUMBER: PCT/US92/07111
 ? FILING DATE: 24-AUG-1992
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/039,457
 ? FILING DATE: 22-APR-1993
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Borun, Michael F.
 ? REGISTRATION NUMBER: 25,447
 ? REFERENCE/DOCKET NUMBER: 31629
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (312) 474-6300
 ? TELEFAX: (312) 474-0448
 ? TELEX: 25-3856
 ? INFORMATION FOR SEQ. ID NO: 17:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 363 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: 1..363
 ? US-08-111-080-17

Query Match 78.1%; Score 257.8; DB 1; Length 363;
 Best Local Similarity 88.0%; Pred. No. 1.2e-78;
 Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

1 GACATTGCTCACCACCAATTCCTCTTGGCTGTGTCTCTAGGAGAGGGCCACC 60
 1 GACATTGCTCACCACCAATTCCTCAGCTTCTTGGCTGTGTCTCTAGGAGAGGGCCACC 60
 61 ATCTCTGCAAGGCCACCAAGTTGATATGATGTGATGATTATG---TGTAC 117
 61 ATATCTCTGAGAGCGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 120
 118 CAACAGAAACGAGAGAGAGCCCAAACTCTCACCATTGCTGATGCTCAATGATAGAT 177
 121 CACAGAAACGAGAGAGAGCCCAAACTCTCATTCTATGATGCTCAACCTAGATATCT 180
 178 GGGATCCAGCAGGTTTATGTCGAGTGGGTCTGGAGACAGCTTCAACCTCAACATCAT 237
 181 GGGGTCCCTCCAGGTTTATGTCGAGTGGGTCTGGAGACAGCTTCAACCTCAACATCAT 240
 238 CCTGTGAGAGAGAGAGTCTTCAACCTTACTGTGACCTTGTATAGATGATCTCTCC 297
 241 CTTGTGAGAGGCTGATGATGCTGCAACCTTACTGTGACCAAAATAGAGAGATCCGCTC 300
 298 ACCTTCGGTGTGGAGACCAAGCTGGAGCTGAAA 330
 301 GCGTTCGGTACTGGAGACCAAGCTGGAGCTGAAA 333

RESULT 14
 US-08-211-980-17
 ? Sequence 17, Application US/08211980
 ? Patent No. 565569
 ? GENERAL INFORMATION:

? APPLICANT: Onno, Tsuneya
 ? TITLE OF INVENTION: HIV Immunotherapeutics
 ? NUMBER OF SEQUENCES: 38
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ? STREET: 6300 Sears Tower, 233 S. Wacker Drive
 ? CITY: Chicago
 ? STATE: Illinois
 ? COUNTRY: USA
 ? ZIP: 60606
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
US-08-211-980-17

Query Match 78.1%; Score 257.8; DB 1; Length 363;
Best Local Similarity 88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 1 GACATTGGCTGCACCAATTCCTCTTGGCTGCTCTAGGCGAGAGGCCACC 60
DB 1 GACATTGGCTGCACCAATTCCTCTTGGCTGCTCTAGGCGAGAGGCCACC 60
QY 61 ATCTCTGCAAGGCGCAAGGTGATTTGATGGTGAATGATG---TGATAC 117
DB 61 ATATCTGCAGAGCCAGTGAAGTGTGATGATGCAATAGTTTATGACATGATC 120
QY 118 CAACGAAACGAGAGCAGCAGCCAACTCTACCTATGCTGATCCCAATCTAGAATCT 177
DB 121 CAGCAGAAACGAGAGCAGTCAACCCCACTCTATGTTGATGCCAATCTAGAATCT 180
QY 178 GGGATCCAGCAGGCTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAATCCAT 237
DB 181 GGGGTCCCTGCGCAGGCTTACGTGGCAGTGGGTCTAGGACAGACTTCACCCCTCAATCCAT 240
QY 238 CCGTGGAGGAGGAGGATGCTGCAACCTATTAATGAGATGAGATCTCC 297
DB 241 CCGTGGAGGAGGATGATGATGCTGCAACCTATTAATGAGATGAGATCTCC 300
QY 298 ACCTGCGTGTGGAGCAGCTGAGCTGAAA 330
DB 301 GCGTTCGCTACTGGGACCAAGCTGAGCTGAAA 333

RESULT 15
PCT-US92-07111-16
Sequence 16, Application PC/TUS9207111
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
Street

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 19920824
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
PCT-US92-07111-16

Query Match 78.1%; Score 257.8; DB 5; Length 363;
Best Local Similarity 88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 1 GACATTGGCTGCACCAATTCCTCTTGGCTGCTCTAGGCGAGAGGCCACC 60
DB 1 GACATTGGCTGCACCAATTCCTCTTGGCTGCTCTAGGCGAGAGGCCACC 60
QY 61 ATCTCTGCAAGGCGCAAGGTGATTTGATGGTGAATGATG---TGATAC 117
DB 61 ATATCTGCAGAGCCAGTGAAGTGTGATGATGCAATAGTTTATGACATGATC 120
QY 118 CAACGAAACGAGAGCAGCAGCCAACTCTACCTATGCTGATCCCAATCTAGAATCT 177
DB 121 CAGCAGAAACGAGAGCAGTCAACCCCACTCTATGTTGATGCCAATCTAGAATCT 180
QY 178 GGGATCCAGCAGGCTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAATCCAT 237
DB 181 GGGGTCCCTGCGCAGGCTTACGTGGCAGTGGGTCTAGGACAGACTTCACCCCTCAATCCAT 240
QY 238 CCGTGGAGGAGGAGGATGCTGCAACCTATTAATGAGATGAGATCTCC 297
DB 241 CCGTGGAGGAGGATGATGATGCTGCAACCTATTAATGAGATGAGATCTCC 300
QY 298 ACCTGCGTGTGGAGCAGCTGAGCTGAAA 330
DB 301 GCGTTCGCTACTGGGACCAAGCTGAGCTGAAA 333

Search completed: September 13, 2003, 06:42:41
Job time : 67 secs

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Db	12	CAGAAACGAGACGACCCAAACTCCTCAACCTATGCTGCATCATCTAGATCTGAGG	180
Qy	181	ATCCCAACGACAGTTTATGTGGCAGTGGTCTGGGACAGACTTCACCTCAACATCATCTT	240
Dp	181	ATCCCAACGACAGTTTATGTGGCAGTGGTCTGGGACAGACTTCACCTCAACATCATCTT	240
Qy	241	GTCGAGAGAGAGATCCTGCACATCTTATACGTACGCTTTTGTATGAGGATCTCCACG	300
Dp	241	GTCGAGAGAGAGATCCTGCACATCTTATACGTACGCTTTTGTATGAGGATCTCCACG	300
Qy	301	TTGCGTCTGGGACCAAGCTGGAGCTGAAA	330
Dp	301	TTGCGTCTGGGACCAAGCTGGAGCTGAAA	330

RESULT 2
115-09-75

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: Sequence 23 Application US/09759112A
: Publication No. US20030100741A1
GENERAL INFORMATION:
APPLICANT: Mueller, Sybille
APPLICANT: Kohler, Heinz
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
: TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
: TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 330
TYPE: DNA
ORGANISM: mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(330)
OTHER INFORMATION: 1F7 VL chain gene
US-09-759-112A-23

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Query Match	100.0%	Score 330;	DB 11;	Length 330;
Best Local Similarity	100.0%	Pred. NO. 2.7e-104;		
Matches 330;	Conservative 0;	Mismatches 0;	Indels 0;	Caps 0

QY	1	GAAATGTGCTCAACCAATTCACACTCTTTGGGTGTCTTAAGGGCAGAGGGCCACC	60
	11		
Db	1	GAAATGTGCTCAACCAATTCACACTCTTTGGGTGTCTTAAGGGCAGAGGGCCACC	60
	61	ATCTCTGCAAGGCCAGCCCAAGTTGATATGATGGTGATAGTTATATGTGTACCA	120
	111		
	61	ATCTCTGCAAGGCCAGCCCAAGTTGATATGATGGTGATAGTTATATGTGTACCA	120
QY	121	CAGAAACCGAGCAGCAGCAACCCAAATCCTCAACTATGTGATATGCATCTAAGATCTGGG	180
	111		
Db	121	CAGAAACCGAGCAGCAGCAACCCAAATCCTCAACTATGTGATATGCATCTAAGATCTGGG	180
	121	CAGAAACCGAGCAGCAGCAACCCAAATCCTCAACTATGTGATATGCATCTAAGATCTGGG	180
	181	ATCCCAAGCCAGGTTTATGTGCAAGTGGGTCTGGGACAGACTTCACCTCAACATTCATCCT	240
	111		
Db	181	ATCCCAAGCCAGGTTTATGTGCAAGTGGGTCTGGGACAGACTTCACCTCAACATTCATCCT	240
	241	GTGGAGAGAGAGATGTGCAACACTTACTAGCTCTTTGATATGAGATCTCCACAG	300
	111		
QY	241	GTGGAGAGAGAGATGTGCAACACTTACTAGCTCTTTGATATGAGATCTCCACAG	300
	111		
Db	241	GTGGAGAGAGAGATGTGCAACACTTACTAGCTCTTTGATATGAGATCTCCACAG	300
	301	TTTCGGTGCTGGGACCAACTGGAGCTGAAA	330
	111		
QY	301	TTTCGGTGCTGGGACCAACTGGAGCTGAAA	330
	111		
Db	301	TTTCGGTGCTGGGACCAACTGGAGCTGAAA	330
	111		

GENERAL INFORMATION:

```

1  APPLICANT: Holmes, Stephen D.
2  Gross, Mitchell S.
3  Sylvester, Daniel R.
4  TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
5  Treatment of IL4 Mediated Disorders
6  NUMBER OF SEQUENCES: 58
7  CORRESPONDENCE ADDRESSES:
8  ADDRESSEE: SmithKline Beecham Corporation
9  STREET: Corporate Intellectual Property, UW2220 - 709
10 Swedeland Rd.
11 CITY: King of Prussia
12 STATE: PA
13 COUNTRY: USA
14 ZIP: 19406-2799
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/879,461
22 FILING DATE: 12-Jun-2001
23 CLASSIFICATION: <Unknown>
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/612,929
26 FILING DATE: <Unknown>
27 APPLICATION NUMBER: US 08/136,783
28 FILING DATE: 14-OCT-1993
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Sulton, Jeffrey A.
31 REGISTRATION NUMBER: 34,028
32 REFERENCE/DOCKET NUMBER: P50186-2
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (215) 270-5024
35 TELEFAX: (215) 270-5090
36 INFORMATION FOR SEQ ID NO: 1:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 396 base pairs
39 TYPE: nucleic acid
40 STRANDEDNESS: double
41 TOPOLOGY: unknown
42 MOLECULE TYPE: CDNA
43 FEATURE:
44 NAME/KEY: CDS
45 LOCATION: 1..396
46 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
47 US-09-879-461-1

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RESULT 3
US-09-879-461-1
; Sequence 1, Application US/09879461
; Publication No. US20020193575A1

[illegible]


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? ORGANISM: Artificial Sequence
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (40)..(753)
? FEATURE:
? NAME/KEY: mat peptide
? LOCATION: (100)..(753)
? FEATURE:
? NAME/KEY: sig peptide
? LOCATION: (40)..(99)
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
? OTHER INFORMATION: encoding the light chain of humanized anti-human
? OTHER INFORMATION: Fas antibody
US-10-216-484-53

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Query Match	83.58;	Score 275.4;	DB 14;	Length 768;
Best Local Similarity	91.38;	Pred. No. 3.6e-85;		
Matches 304;	Conservative 0;	Mismatches 26;	Indels 3;	Gaps 1

RESULT 7
US-10-216-484-51
Sequence 51, Application US/10216484
Publication No. US20030103976A1

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? LOCATION: (100)..(753)
? FEATURE:
? NAME/KEY: sig peptide
? LOCATION: (40)..(99)
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Desined DNA
? OTHER INFORMATION: encoding the light chain of humanized anti-human
? OTHER INFORMATION: Fas antibody
US-10-216-484-51

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Query Match	82.5%	Score 272.2;	DB 14;	Length 768;
Best Local Similarity	90.7%;	Pred. No. 4.6e-84;		
Matches 302; Conservative	0;	Mismatches 28;	Indels 3;	Gaps 1

Db	340	CGTGTGAGAGAGAGGATCTGCAACCTATTACTGTCAAGAAAGTAATAGAGATCTTCGG	399
Oy	298	ACGTTGGTGCTGGGACCAAGCTGGAAGCTGAAA	330
Db	400	ACGTTGGTGCAAGGCCACAGGCTGGAAATCAAA	432

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: SEQ_ID NO 51
: LENGTH: 768
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (40)..(753)
: FEATURE:
: NAME/KEY: mat peptide

```

```

? ORGANISM: Artificial Sequence
?
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (40)..(753)
?
? FEATURE:
? NAME/KEY: mat peptide
? LOCATION: (100)..(753)
?
? FEATURE:
? NAME/KEY: sig peptide
? LOCATION: (40)..(99)
?
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Designed DNA

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Query Match	82.5%	Score 272.2;	DB 12;	Length 825;
Best Local Similarity	90.7%	Pred. No. 4.7e-84;		
Matches 302;	Conservative	0;	Mismatches 28;	Indels 3; Gaps 1

OY GACATGTGCTCACCAATTCTCAGCTCTTTGGCTGTCTCAAGGCGAAGGGCCACC 60
Db 73 GACATTGTGCTGCACCAATCTCAGCTTCTTGGCTGTCTCAAGGCGAAGGGCCACC 132
OY 61 ATCTCTGCAAGGCCCAAGTGTGATTATGATGTTGTAATGTA---TGCTAC 117


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1  TITLE OF INVENTION: Anti-Fas Antibodies
2  FILE REFERENCE: 980126CJP/HG
3  CURRENT APPLICATION NUMBER: US/10/216,484
4  CURRENT FILING DATE: 2002-08-09
5  PRIOR APPLICATION NUMBER: US/09/499,662
6  PRIOR FILING DATE: 2000-02-09
7  PRIOR APPLICATION NUMBER: US 09/053,583
8  PRIOR FILING DATE: 1998-04-01
9  NUMBER OF SEQ ID NOS: 165
10 SEQ ID NO 49
11 LENGTH: 768
12 TYPE: DNA
13 ORGANISM: Artificial Sequence
14 FEATURE:
15 NAME/KEY: CDS
16 LOCATION: (40)..(753)
17 FEATURE:
18 NAME/KEY: mat peptide
19 LOCATION: (100)..(753)
20 FEATURE:
21 NAME/KEY: sig peptide
22 LOCATION: (40)..(99)
23 FEATURE:
24 OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
25 OTHER INFORMATION: encoding the light chain of humanized anti-human
26 US-10-216-484-49

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Query Match	77.28	Score	254.6	DB	14	Length	768
Best Local Similarity	87.48	Pred. NO.	6e-78				
Matches	291	Conservative	0	Mismatches	39	Indels	3
						Gaps	1

OY	GACATTTGTGTCACCAATTTCTCCAGTTTGTGGTGTGTCCTAAGGACCAAGGGCCACC	60
Db	100 GACATTTGTGTCACCAATCTCCAGTACTTTGTCTGTCTCCAGGGAGAGGGCCACC	158
OY	61 ATTCCTCGCAAGCCACGCCAAAGTGTGATTATGATGCTGATAGTTATATG--TGGTAC	117
Db	160 CTCTCTCGCAAGCCACGCCAAAGTGTGATTATGATGCTGATAGTTATATCAATCGGTAC	219
OY	118 CAACAGAAACCAAGACAGGCCACCCAAACCTCCACCTATAGCGATCCATCAATGTGATCT	177
Db	220 CAACAGAAACCAAGACAGGCCACCCAGACCTCCATCAATGTGATCCATCAATGTGATCT	279
OY	178 GGGATCCCAACAGGTTTATGTGGCAAGTGGGTCTGGGACAGACTTCACCTTCACATTCAT	237
Db	280 GGGATCCCAACAGGTTTATGTGGCAAGTGGGTCTGGGACAGACTTCACCTTCACATTCAT	339
OY	238 CCGTGTGAGAGAGAGATGCTCTCAACCTATTACTCTCAGCTTTGTAATGAGATCTCCG	297
Db	340 CGTCTGGAGCGCGCGGATTTTGCAGTCTATTACTGTCAAGCAAGTAATGAGATCTCTCG	399
OY	298 ACGTTGGGTCTGGGACCAAGCTGGAAGCTGAAGA	330
Db	400 ACGTTGGGTCAAGGACCAAGCTGGAAGTAACAA	432

RESULT 14
US-10-171-452A-37
Sequence 37, Application US/10171452A
Publication No. US20030108518A1
GENERAL INFORMATION:
APPLICANT: Frewin, Mark
APPLICANT: Waldmann, Herman
APPLICANT: Gorman, Scott
APPLICANT: Hale, Geoff
APPLICANT: Rao, Patricia
APPLICANT: Kornaga, Tadeusz
APPLICANT: Ringler, Douglas
APPLICANT: Cobbold, Stephen
APPLICANT: Minsor-Hines, Dawn
TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
FILE REFERENCE: 695458-59

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: CURRENT APPLICATION NUMBER: US/10/111,452A
: CURRENT FILING DATE: 2003-02-10
: PRIOR APPLICATION NUMBER: US60/373,471
: PRIOR FILING DATE: 2002-04-18
: PRIOR APPLICATION NUMBER: US60/373,470
: PRIOR FILING DATE: 2002-04-18
: PRIOR APPLICATION NUMBER: US60/345,194
: PRIOR FILING DATE: 2002-10-19
: PRIOR APPLICATION NUMBER: GB0122724.8
: PRIOR FILING DATE: 2001-09-20
: PRIOR APPLICATION NUMBER: GB0114517.6
: PRIOR FILING DATE: 2001-06-14
: NUMBER OF SEQ ID NOS: 60
: SEQ ID NO 37
: LENGTH: 717
: TYPE: DNA
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: DNA Sequence encoding light chain of humanized antibody
US-10-171-452A-37

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Query Match	76.7%	Score 253;	DB 14;	Length 717;
Best Local Similarity	87.1%	Pred. No. 2.1e-77;		
Matches 290; Conservative	0;	Mismatches 40;	Indels 3;	Gaps 1

QY	1	GACATTGTGCTCCACCAATCTCCAGCTCTTGGCTGTGCTCTAGGGACAGGGCCACC	60
Db	61	GACATTGTGATGACCCCAATCTCCAGATTCTTTGGCTGTGCTCTAGTGAAGAGGGCCACC	120
QY	61	ATCTCTCGCAAGGCCACGACCAAGTGTGATTATGATGTGATAGTTATATG---TGGTAC	117
Db	121	ATCAACTCGCAAGGCCACGACCAAGTGTGATTATGATGTGATAGTTATATGCAACTGTAT	180
QY	118	CAACAGAAACACAGGACAGCCACCCAAACCTCTCAGCTATGCTGCATCCATCTAGAACTCT	177
Db	181	CACAGAAACACAGGACAGCCACCCAAACCTCTCATCTATGTTGCATCCAACTGAGACTCT	246
QY	178	GGGATCCCAAGCCAGTTTAACTGAGTGGGCTGTGGGACAGACTTCACCCCTAACATCAT	237
Db	241	GGGGTCCCAAGACAGTTTAACTGAGTGGGCTGTGGGACAGACTTCACCCCTAACATCAT	300
QY	238	CCCTGTGGAGAGAGAGGATCTCTCAACCTAATTAAGTCTGAGCTTTGATATGAAGATCTCC	297
Db	301	TCTCTCAGAGCGGAGGATGTTGCAGTCTAATTAAGTCTGAGCAAGATCTTCAGGACCTCCG	366
QY	298	ACGTTGGGTCTGGAGCAACGCTGGAGCTGAAA	330
Db	361	ACGTTGGGTGAGAGTCAAGGCTGAGAAATCAAA	393

RESULT 15
US-10-171-452A-43
Sequence 43: Application US/10/171452A
Publication NO. US20030108518A1
GENERAL INFORMATION:
APPLICANT: Frewin, Mark
APPLICANT: Waldmann, Herman
APPLICANT: Gorman, Scott
APPLICANT: Hale, Geoff
APPLICANT: Rao, Patricia
APPLICANT: Kornaga, Tadeusz
APPLICANT: Ringler, Douglas
APPLICANT: Cobbold, Stephen
APPLICANT: Winstor-Hines, Dawn
TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
FILE REFERENCE: 695458-59
CURRENT APPLICATION NUMBER: US/10/171,452A
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US60/373,471
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US60/345,194

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 04:56:01; Search time 2855 Seconds

(without alignments)
4728.608 Million cell updates/sec

Title: US-09-759-112a-23

Perfect score: 330

Sequence: 1 gacatgagctaccacattc.....ggaccacagctgagctgaa 330

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

al number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenBank: *
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30: em_htg_hum: *
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32: em_htg_other: *
33: em_htg_mus: *
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35: em_htg_rnd: *
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293	88.8	333	6 E30643	E30643 Antibody an
2	293	88.8	363	6 MUSL2021IK	M97869 Mouse hybr
3	293	88.8	714	6 BD090542	BD090542 Drug cont
4	293	88.8	714	6 BD090651	BD090651 Drug cont
5	293	88.8	714	6 E40005	E40005 Drug cont
6	293	88.8	714	6 E40813	E40813 Humanized a
7	293	88.8	714	6 E43359	E43359 Humanized a
8	293	88.8	877	6 E31225	E31225 Device for
9	293	88.8	925	6 E30616	E30616 Antibody an
10	293	88.8	925	6 E30617	E30617 Antibody an
11	289.8	87.8	354	10 MUSL71IGKV	M97875 Mouse hybr
12	289.8	87.8	363	10 MUSL931GKV	M97879 Mouse hybr
13	289.8	87.8	393	10 AF045518	AF045518 Mus muscu
14	288.2	87.3	333	6 E07408	E07408 cDNA encodi
15	288.2	87.3	333	6 MMA005355	AJ005355 Mus muscu
16	288.2	87.3	363	10 MUSL341GKV	M97871 Mouse hybr
17	286.6	86.8	333	6 AR014069	AR014069 Sequence
18	286.6	86.8	333	6 S54207	S54207 V kappa 21-
19	286.6	86.8	831	6 AX392999	AX392999 Sequence
20	286.2	86.7	350	10 MUSIGKABBC	M92401 Mouse Ig Ka
21	285	86.4	333	10 MUSIGLSB	M80406 Mouse Igl c
22	285	86.4	333	10 S42888	S42888 Ig V kappa
23	285	86.4	334	6 E02169	E02169 DNA encodin
24	285	86.4	336	10 NMIGLC310	X65091 M.musculus
25	285	86.4	336	10 NMIGLC404	X65092 M.musculus
26	285	86.4	393	10 S30265	S30265 Ig VL-antl-
27	285	86.4	396	10 AF207705	AF207705 Mus muscu
28	285	86.4	744	12 AF402256	AF402256 Synthetic
29	283.6	85.9	333	10 AY173024	AY173024 Mus muscu
30	283.4	85.9	333	10 AF112403	AF112403 Mus muscu
31	283.4	85.9	333	10 AF321952	AF321952 Mus muscu
32	283.4	85.9	336	10 MUSIGKAAW	M31962 Mouse Ig re
33	283.4	85.9	393	6 AR144017	AR144017 Sequence
34	281.8	85.4	336	10 MM0012372	AJ012372 Mus muscu
35	280.8	85.1	360	10 MUSIGKAF	M61046 Mus musculu
36	280.8	85.1	900	6 I08223	I08223 Sequence 1
37	277.6	84.1	351	10 MUSIGKABH	M92406 Mouse Ig ka
38	276	83.6	333	10 MMVLE10	X51854 Mouse mRNA
39	276	83.6	353	10 MUSIGKABD	M92402 Mouse Ig ka
40	275.4	83.5	336	10 NMIGLC413	X65093 M.musculus
41	275.4	83.5	768	6 BD090559	BD090559 Drug cont
42	275.4	83.5	768	6 BD090668	BD090668 Drug cont
43	275.4	83.5	768	6 E40022	E40022 Drug cont
44	275.4	83.5	768	6 E40830	E40830 Humanized a
45	275.4	83.5	768	6 E43376	E43376 Humanized a

ALIGNMENTS

RESULT 1
LOCUS E30643 333 bp DNA linear PAT 18-JUN-2001
DEFINITION Antibody and nucleic acid encoding the same.
ACCESSION E30643.1 GI:13017209
VERSION E30643.1
KEYWORDS JP 1999332563-A/30.
SOURCE Mus sp.
ORGANISM Mus sp.

REFERENCE
AUTHORS Mitsuhashi, O., Takayuki, K. and Ikuno, M.
TITLE Antibody and nucleic acid encoding the same
JOURNAL Patent: JP 1999332563-A 30 07-DEC-1999;

Pred. No. is the number of results predicted by chance to have a

COMMENT	OS	Mus sp. (mouse)	ASAH1 CHEM IND CO LTD
PN	JP 1999332563-A/30		
PD	07-DEC-1999		
PF	26-MAY-1998		
PR	1998165034		
PI	MITSUHARU ONO, TAKAYUKI KUSAKA, IKUO MORIMOTO		
PC	C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08		
PC	C12N15/00,		
PC	C12N15/00,		
CC	Strandedness: Double;		
CC	Topology: Linear;		
FT	key	1.333	
FT	source	/organism="Mus sp. (mouse)"	
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GIN	Query Match	88.8%; Score 293; DB 6; Length 333;	
GIN	Best Local Similarity	4.6%; Pred. No. 1, 1e-88;	
GIN	Matches	315; Conservative 0; Mismatches 15; Indels 3; Gaps 1	
GIN	1	GACATTGTCACCAATCTTCACAGCTTCTTTGGCTGTCTCTAGGCGAGGGCCACC	60
GIN	1	GACATTGTCACCAATCTTCACAGCTTCTTTGGCTGTCTCTAGGCGAGGGCCACC	60
GIN	61	ATTCCTCTGAGGCGCCAGCCCAAGTGTATATATGATGATAGTATATG--TGCTAC	117
GIN	61	ATTCCTCTGAGGCGCCAGCCCAAGTGTATATGATGATAGTATATG--TGCTAC	117
GIN	118	CAACAGAAACAGGACGACGACCAACCTCCACCTAGTGGATGATGACCAATCTAGATCT	177
GIN	121	CAACAGAAACAGGACGACGACCAACCTCCACCTAGTGGATGATGACCAATCTAGATCT	180
GIN	178	GGGATCCAGGACGAGTTTATGAGGAGTGGGCTGTGGAGACAGATCCCTCAACATCCAT	237
GIN	181	GGGATCCAGGACGAGTTTATGAGGAGTGGGCTGTGGAGACAGATCCCTCAACATCCAT	240
GIN	238	CCTGTGGAGGAGGAGATGCTGCAACCTATTACTGTCAAGCTTTGTAATGAGGATCTCTCC	297
GIN	241	CCTGTGGAGGAGGAGATGCTGCAACCTATTACTGTCAAGGATGAGGATCTCTCG	300
GIN	298	ACGTTGGTGGTGGGACCAAGCTGGAGGTGA	330
GIN	301	ACGTTGGTGGGACCAAGCTGGAGGTGA	333
RESULT 2	MUSL2021GK	363 bp	linear
DEFINITION	Mus hybridoma Ig rearranged kappa-chain mRNA V-region, partial cds.		
ACCESSION	M97869.1		
VERSION	GI:198667		
KEYWORDS	V-region; Immunoglobulin light chain; Immunoglobulin-kappa; processed gene.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 363)		
TITLE	Lothman,K.L., Buck,D.W., Garrillo,M.A. and Kennedy,R.C.		
JOURNAL	Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence		
COMMENT	Unpublished (1992)		
FEATURES	Original source text: Mus musculus (strain BALB/c, sub-species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.		
FEATURES	Location/Qualifiers		

	source	1. .363 /organism="Mus musculus" /mol_type="mRNA" /strain="BALB/c" /sub_species="domesticus" /db_xref="taxon:10090" /map="6" /tissue_type="SP20-BALB/c fusion hybridoma"
	gene	1. .363 /gene="Irk" (1.11) . .363 /gene="Irk" /standard_name="L202; monoclonal antibody (CD4 antigen specificity)"
	V-region	.
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	Query Match	88.8%; Score 293; DB 10; Length 363;
	Best Local Similarity	94.6%; Pred. No. 1.le-89;
	Matches 315:	Conservative 0; Mismatches 15; Indels 3; Gaps 1;
OY	1	GACATTGTGCTCACCAATTCGCAGCTTCTTGCGTGCTGTCTCAGAGGAGGCCACC 60
Dd	1	GACATTGTGCTGACCCCATCTCCAGCTCTTTGGCTGTCTCTAAGGACAGGCCACC 60
OY	61	ATCTCTGTGAAGGCCAACAGTGTGATTATGATGTGTAATGATTATG--TGTTAC 117
Dd	61	ATCTCTGTGAAGGCCAACAGTGTGATTATGATGTGTAATGATTATGACTGTCAC 120
OY	118	CACAGAACAACGAGACAGCCACCCCACAACTCTCCACCTTGTGTCATCCCATCTGAATCT 177
Dd	121	CACAGAACAACGAGACAGCCACCCCACAACTCTCTATCTATGCTGATCCAAATCTGAATCT 180
OY	178	GGGATCCCCAGCAGAGTTTAGTGAGCAGTGGTCTGGAGACAGACTTCACCCCTGACATCCAT 237
Dd	181	GGGATCCCCAGCAGAGTTTAGTGAGCAGTGGTCTGGAGACAGACTTCACCCCTGACATCCAT 240
OY	238	CCTGTGGAGAGGAGAGATGCTGCACAACCTATTACTGTCACTTTGTAATGAGCATCTCCC 297
Dd	241	CCTGTGGAGAGGAGAGATGCTGCACAACCTATTACTGTCAAGCAAAGTAATACGATCTCCC 300
OY	298	ACGTTGGTGCTGGAGCCAACGCTGGAGCGTGA 330
Dd	301	ACGTTGGAGGGGGAGCCAGCTGAGATAAAA 333
RESULT 3	BD090542	714 bp DNA linear PAT 27-AUG-2002
LOCUS	BD090542	
DEFINITION	Drug containing humanized anti-Fas antibody.	
ACCESSION	BD090542.1	GI:22636152
VERSION	BP 2001342148-A/2.	
KEYWORDS	JP 2001342148-A/2.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 714) Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I. Drug containing humanized anti-Fas antibody Patent: JP 2001342148-A 2 11-DEC-2001;	
AUTHORS	TAMAKI	
TITLE	PC A6IK39/395,A6IK38/00,A6IP1/16,A6IP7/06,A6IP9/00,A6IP9/10, PC A6IP13/12, PC A6IP19/02,A6IP29/00,A6IP37/00,A6IP37/06,A6IP37/08,A6IP43/00// PC C12N15/02, PC A6IK37/02,C12N15/00	
JOURNAL	PI NOBFUTS SERIZAWA,HIDEYUKI HARIYAMA,KORI MAKAHARA, IKUO PI	
COMMENT	OS Mus musculus (mouse) PN JP 2001342148-A/2 PD 11-DEC-2001 PF 28-MAR-2001 JP 2001093106 PT NOBFUTS SERIZAWA,HIDEYUKI HARIYAMA,KORI MAKAHARA, IKUO PI	

CC Drug containing humanized anti-Fas antibody
 FH Key Location/Qualifiers
 FT CDS (1)..(714)
 FT mat_peptide (61)..(714)
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BASE COUNT 200 a 184 c 173 g 157 t

ORIGIN

Query Match 88.8%; Score 293; DB 6; Length 714;
 Best Local Similarity 94.6%; Pred. No. 1.2e-88;
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 1 GACATTGTCCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGGCCACC 60
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 61 GACATTGTCCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGGCCACC 120
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 61 ATCTCTCGAAGCCCAAGAGTGTGATTATGATGATAGTTATG--TGGTAC 117
 ||||||||| |||||||||||||||||||||||||||||||||||
 121 ATCTCTCGAAGCCCAAGAGTGTGATTATGATGATAGTTATG--TGGTAC 180
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 QY 118 CAACAGAAACGAGCAGCCACCAACTCTCACCCTATGTCATCCATCTAGAAATCT 177
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 QY 298 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAA 330
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 Db 361 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAA 393
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RESULT 4
 BD090651 714 bp DNA linear PAT 27-AUG-2002
 LOCUS Drug containing humanized anti-Fas antibody.
 DEFINITION
 ACCESSION BD090651.1 GI:22636261
 VERSION BD090651.1
 KEYWORDS JP 2001342149-A/2.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 714)
 Takahashi, W., Haruyama, H. and Serizawa, N.
 Drug containing humanized anti-Fas antibody
 Patent: JP 2001342149-A 2 11-DEC-2001;
 SANKYO CO LTD
 OS Mus musculus (mouse)
 PN JP 2001342149-A/2
 PD 11-DEC-2001
 PE 28-MAR-2001 JP 2001093243
 PI WATARU TAKAHASHI, HIDEYUKI HARUYAMA, NOBUFUSA SERIZAWA, PI
 A61K39/395, A61K39/395, A61P1/16, A61P7/06, A61P9/00, A61P9/10, PC
 A61P13/12,
 PC A61P17/00, A61P31/14, A61P31/18, A61P31/20, A61P37/00, A61P37/06,
 PC A61P37/08,
 PC A61P43/00//C12N15/02, C12N15/00
 CC Drug containing humanized anti-Fas antibody
 FH Key Location/Qualifiers
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 FT mat_peptide (61)..(714)
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BASE COUNT 200 a 184 c 173 g 157 t

ORIGIN

Query Match 88.8%; Score 293; DB 6; Length 714;
 Best Local Similarity 94.6%; Pred. No. 1.2e-88;
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 1 GACATTGTCCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGGCCACC 60
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 Db 61 GACATTGTCCTCACCATTCTCCAGCTTCTTGGCTGTCTCTAGGCGAGGGCCACC 120
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 QY 61 ATCTCTCGAAGCCCAAGAGTGTGATTATGATGATAGTTATG--TGGTAC 117
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 Db 121 ATCTCTCGAAGCCCAAGAGTGTGATTATGATGATAGTTATG--TGGTAC 180
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 QY 118 CAACAGAAACGAGCAGCCACCAACTCTCACCCTATGTCATCCATCTAGAAATCT 177
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 Db 181 CAACAGAAACGAGCAGCCACCAACTCTCACCCTATGTCATCCATCTAGAAATCT 240
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 Db 301 CCGTGGAGGAGAGATGCTGCACCTTATCTGTCACCTTGTATAGAGATCCTCC 360
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 QY 298 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAA 330
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RESULT 5
 E40005 714 bp DNA linear PAT 31-JAN-2002
 LOCUS Drug containing anti-Fas antibody.
 DEFINITION
 ACCESSION E40005
 VERSION E40005.1 GI:18627121
 KEYWORDS JP 2000169393-A/2.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 714)
 Serizawa, N., Haruyama, H., Takahashi, W., Yoshida, H., Ichikawa, K.,
 Okuma, J., Otsuki, M., Shiraiishi, A. and Yonehara, S.
 Drug containing anti-Fas antibody
 Patent: JP 2000169393-A 2 20-JUN-2000;
 SANKYO CO LTD
 OS Mus musculus (mouse)
 PN JP 2000169393-A/2
 PD 20-JUN-2000
 PE 30-SEP-1999 JP 1999278301
 PR
 PI NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, WATARU TAKAHASHI, PI
 HIROKO YOSHIDA,
 PI KIMIHISA ICHIKAWA, JUN OKUMA, MASAHIKO OTSUKI, AKIO SHIRAIISHI, PI
 SHIN YONEHARA
 PC A61K39/395, A61K39/395, A61K39/00, A61P1/16, A61P7/06, A61P9/00, PC
 A61P9/10,
 PC A61P13/12, A61P31/18, A61P37/06, C12N5/10, C12N15/02, C12N15/09, PC
 C12P21/08//
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 CC
 FH Key Location/Qualifiers
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 FT mat_peptide (61)..(714)
 FT sig_peptide (1)..(60).

FEATURES	source	Location/Qualifiers
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	/mol_type="genomic DNA"	
	/db_xref="taxon:10090"	
BASE COUNT	200 A 184 C 173 G 157 T	
ORIGIN		
Query Match	88.8%; Score 293; DB 6; Length 714;	
Best Local Similarity	94.6%; Pred. No. 1.2e-88;	
Matches 315; Conservative	0; Mismatches 15; Indels 3; Gaps 1	
OY	1 GACATTGGCTCACCATTTCCTCCACTTCTTGCGTGTGCTCTAGGCAGAGGGCCACC 60	
DB		
OY	61 GACATTTGGCTGACCAACAATCTCCACTTCTTGCGTGTGCTCTAGGGCAGAGGGCCACC 120	
DB		
OY	61 ATCTCTCTCAAGGCCAGCCAAAGTGTGATTATGATGGTAGTATATATG--TGGTAC 117	
DB		
OY	121 ATCTCTCTCAAGGCCAGCCAAAGTGTGATTATGATGGTAGTATATATGAACGTGAC 180	
DB		
OY	118 CAACGAAACCAGACAGCACCCAACTCCTCAGCTTATGCTGCATCCANTAGAACT 177	
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OY	181 CAACGAAACCAGACAGCACCCAACTCCTCAGCTTATGCTGCATCCANTAGAACT 240	
DB		
OY	178 GGATATCCAGCAGCATGTTATAGTGGCAGTGGTGGGAGACAGCTTACCCTCAACATCCAT 237	
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OY	241 GGGATCCAGCAGCATGTTATAGTGGCAGTGGTGGGAGACAGCTTACCCTCAACATCCAT 300	
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OY	238 CCTGTGAGAGAGAGAGATGCTGCACACTATTACTGTGACGTTTTGTAATGAGAGATCCTCC 297	
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DB		
OY	298 ACCTTCCGCTGCTGGACCACTGGAGCTGAAA 330	
DB		
OY	361 ACCTTCCGCTGCTGGACCACTGGAGCTGAAA 393	
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LOCUS	E40813	714 bp DNA linear PAT 31-JAN-2002
DEFINITION	Humanized anti-Fas antibody.	
ACCESSION	E40813	
VERSION	E40813.1 GI:18627390	
KEYWORDS	JP 200016574-A/2.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 714) Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I. Humanized anti-Fas antibody Patent: JP 200016574-A 2 20-JUN-2000; SANKYO CO LTD	
TITLE	HUMANIZED ANTI-FAS ANTIBODY	
AUTHORS	SERIZAWA N, HARUYAMA H, NAKAHARA K, TAMAKI I	
JOURNAL	SANKYO CO LTD	
COMMENT	OS Mus musculus (mouse) PN JP 200016574-A/2 PD 20-JUN-2000 PF 29-SEP-1999 JP 1999275441	
	PR NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKUO TAMAKI	
	PI C12N5/09,A61K39/00,A61K39/395,A61P37/02,A61P43/00,	
	PC C07K16/18	
	PC C12N1/21,C12N5/10,C12P21/08//((C12N1/21,C12R1:19),C12N15/00, PC	
	C12N5/00	
CC		
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[illegible][illegible]

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QY	238	CCTGTGAGGAGGAGGAGTGTCTGCAACCTATTACTGTCAAGCTTTGTATAGAGGATCCTCC	297
Db	307	CCTGTGAGGAGGAGGAGTGTCTGCAACCTATTACTGTCAAGGAAAGTATGAGGATCCTCCG	366
QY	298	ACGTTCCGTCCTGGGACCAACCTGGAGCTGAAA	330
Db	367	ACGTTCCGTCCTGGGACCAACCTGGAGGAAATCAAA	399
RESULT	10		
LOCUS	E30617	925 bp	DNA
DEFINITION	Antibody and nucleic acid encoding the same.	linear	PAT 18-JUN-2001
ACCESSION	E30617		
VERSION	E30617.1	GI:13017183	
KEYWORDS	JP 1999332563-A/4.		
ORIGIN	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 925)		
TITLE	Mitsuharu, O., Takayuki, K. and Ikuno, M.		
JOURNAL	Antibody and nucleic acid encoding the same		
COMMENT	Patent: JP 1999332563-A 4 07-DEC-1999;		
	ASAHI CHEM IND CO LTD		
	OS Mus sp. (mouse)		
	PN JP 1999332563-A/4		
	PD 07-DEC-1999		
	PF 26-MAY-1998 JP 1998163034		
	PR		
	PI MITSUHANU ONO, TAKAYUKI KUSANA, IKUNO MORIMOTO		
	PC C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08,		
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	PC C12N15/00,		
	CC Strandedness: Double;		
	CC Topology: Linear;		
	CC FH key		
	Location/Qualifiers		
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			Gaps 1;
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QY	61	ATCTCTGCGCAAGGCCACCAAAAGTGTGATTTATGATGGTGAATGATATG--TGGTAC	117
Db	526	ATCTCTGCGCAAGGCCACCAAAAGTGTGATTTATGATGGTGAATGATGAACTGTTAC	585
QY	118	CAACAGAAACAGGACGACCAACCACTCTCTACACTATGCTGCATCCAACTAGAACT	177
Db	586	CAACAGAAACAGGACGACCAACCACTCTCTACACTATGCTGCATCCAACTAGAACT	645
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Db	646	GGGATCCAGCAGAGTTTAAAGTGGCGAGTGGGCTGGGACAGACTTCACCTCAACATTCAT	705
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[illegible]

ACCESSION	region, (Igrk) mRNA, partial cds.
AF045518	
AF045518.1	GI:2906119
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	Mus musculus (house mouse)
REFERENCE	
AUTHORS	Mus musculus
TITLE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
REFERENCE	Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies
TITLE	Unpublished
JOURNAL	2 (bases 1 to 393)
REFERENCE	O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
TITLE	Direct Submission
JOURNAL	Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
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Best Local Similarity	94.08; Pred. No. 1.4e-87;
Matches 313; Conservative	0; Mismatches 17; Indels 3; Gaps 1;
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QY	61 ATCTCTGCAAGGCCAACAAAGTGTGATTTAGATGGTATATATG--TGGTAC 117
Db	
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QY	118 CACACGAAGAACAGAGACAGCCACCAACCTCTCCTCATCTGATGCATCAATCTGATCT 177
Db	
181 CACACGAAGAACAGAGACAGCCACCAACCTCTCCTCATCTGATGCATCAATCTGATCT 240	
QY	178 GGGATCCACACAGAGTTTAAATGGCAGAGGCTCTGGACAGACTTCACCCCTCAACATCAT 237
Db	
241 GGGATCCACACAGAGTTTAAATGGCAGAGGCTCTGGACAGACTTCACCCCTCAACATCAT 300	
QY	238 CTTGTGAGAGAGAGATGCTGCACCTATTTACTGTGAGCTTTGTAAATGAGATCTCC 297
Db	
301 CTTGTGAGAGAGAGATGCTGCACCTATTTACTGTGAGCAAAAGTAAATGAGATCTCC 360	
QY	298 ACGTTGCTGCTGGAGCAACAGCTGAGCTGAAA 330

[illegible]

QY	298	ACGTTCCGCTGCTGGACCAAGCTGAGCTGAAA	330
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RESULT 15			
LOCUS	MAA005355	333 bp	mRNA
DEFINITION	Mus musculus immunoglobulin variable light chain region.		
ACCESSION	AJ005355		
VERSION	AJ005355.1	GI:3046765	
KEYWORDS	immunoglobulin; light chain; variable region.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 Monnet,C., Laune,D., Laroche-Traïneau,J., Biard-Piechaczyk,M., Briant,L., Bes,C., Pugnieri,M., Mani,J.C., Pau,B., Cerutti,M., Devauchelle,G., Devaux,C., Granier,C. and Charles,T.		
TITLE	Synthetic peptides derived from the variable regions of an anti-CD4 monoclonal antibody bind to CD4 and inhibit HIV-1 promoter activation in virus-infected cells		
JOURNAL	J. Biol. Chem. 274 (6), 3789-3796 (1999)		
MEDLINE	99121124		
PUBMED	9920932		
REFERENCE	2		
AUTHORS	Monnet,C., Laune,D., Laroche-Traïneau,J., Piechaczyk,M., Pugnieri,M., Mani,J.C., Pau,B., Cerutti,M., Devauchelle,G., Devaux,C., Granier,C. and Charles,T.		
TITLE	Synthetic peptides designed from the variable regions of an anti-CD3 like monoclonal antibody bind to CD4 and inhibit HIV promoter activity		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 333)		
AUTHORS	Charles,T.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-APR-1998) Char��s T., Faculte de Pharmacie, CNRS UMR 9921, 15 Avenue Charles Flahault - Montpellier, 34060, FRANCE		
FEATURES	Location/Qualifiers		
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BASE COUNT	87 a 85 c 86 g 75 t		
ORIGIN			
Query Match	87.3%. Score 288.2; DB 10; Length 333; Best Local Similarity 93.7%; Pred. No. 5e-87;		
Matches	312; Conservative 0; Mismatches 18; Indels 3; Gaps 1		
QY	1	GACATTTGCTGCACCAATTCCTCCAGCTTCTTGCTGCTGCTCTGAGGACAGGGCCACC	60
Db	1	GACATTTAGCTCACCCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGACAGGGCCACC	60
QY	61	ATCCCTCGCAAGGCGACCCAAAGTGTGATTATGATGGTATAGTTATATG--TGGTAC	117
Db	61	ATCTCCGCAAGGCGACCCAAAGTGTGATTATGATGGTATAGTTATATGACGCTAC	120
QY	118	CAACAGAACCGAGACAGCCACCACCAACTCTCTACCTATGCTGATCCCAATCTAGAATCT	177
Db	121	CAACAGAACCGAGACAGCCACCACCAACTCTCTATCTATGCTGATCCCAATCTAGAATCT	180
QY	178	GGGATCCCGACGAGTTTATGCGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT	237
Db	181	GGGATCCCGACGAGTTTATGCGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT	240

Qy 238 CCTGTGAGAGAGAGATGCTGCAACCTATTACTGTGACGCTTGTATGAGGATCCTCCC 297
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Db 241 CCTGTGAGAGAGAGATGCTGCAACCTATTACTGTGACGCAAGTATGAGGATCCTGCG 300
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Qy 298 ACCTTCGCTGCTGGACCAAGCTGGAGCTGAAA 330
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Db 301 ACCTTCGCTGAGGACCAAGCTGGAAATCAAA 333
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Job time : 2867 secs

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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:39:02 ; Search time 13.05 Seconds
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Title: US-09-759-112a-36

Perfect score: 54

Sequence: 1 OLCNEDPPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	38	70.4	9	2	US-08-483-636-20
3	38	70.4	9	2	US-08-483-632-20
4	38	70.4	111	2	US-08-483-636-73
5	38	70.4	111	2	US-08-483-632-73
6	38	70.4	131	1	US-08-137-117D-33
7	38	70.4	131	2	US-08-436-717-33
8	38	70.4	131	2	US-08-621-751A-10
9	38	70.4	131	2	US-08-621-751A-14
10	38	70.4	131	2	US-08-483-636-58
11	38	70.4	131	2	US-08-483-632-58
12	38	70.4	132	2	US-08-483-632-2
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17	36	66.7	77	2	US-08-486-397-4
18	36	66.7	77	2	US-08-486-397-4
19	36	66.7	77	2	US-08-486-399-4
20	36	66.7	77	2	US-08-486-399-4
21	36	66.7	77	2	US-08-461-965-4
22	36	66.7	77	2	US-08-461-965-4
23	36	66.7	77	2	US-08-326-110A-33
24	36	66.7	77	2	US-08-634-641-4
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29	36	66.7	77	3	US-09-249-472-40	Sequence 40, Appli
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ALIGNMENTS

RESULT 1
US-08-984-277-7
Sequence 7, Application US/08984277
Patent No. 6057421
GENERAL INFORMATION:
APPLICANT: Muller, Sybille
APPLICANT: Kohler, Heinz
TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE MONOCLONAL ANTIBODY 1F7
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,277
FILING DATE: 3-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bucca, Daniel
REGISTRATION NUMBER: 42,368
REFERENCE/DOCKET NUMBER: 50200-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8600
TELEFAX: 202-756-8699
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-984-277-7
Query Match 100.0%; Score 54; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 QLCNEDPPT 18

RESULT 2

US-08-483-636-20

Sequence 20, Application US/08483636

Patent No. 5914110

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.

APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

TITLE OF INVENTION: Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P.O. Box 1539 / UM2220

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,636

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117366

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/136783

FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 07-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50186-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-636-20

Query Match 70.4%; Score 38; DB 2; Length 9;

Best Local Similarity 77.8%; Pred. No. 2.5e+05;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 QQSNEDPPT 9

RESULT 3

US-08-483-632-20

Sequence 20, Application US/08483632

Patent No. 5928904

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.

APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

TITLE OF INVENTION: Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P.O. Box 1539 / UM2220

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,632

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117366

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/136783

FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 07-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50186-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-632-20

Query Match 70.4%; Score 38; DB 2; Length 9;

Best Local Similarity 77.8%; Pred. No. 2.5e+05;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9

Db 1 QQSNEDPPT 9

RESULT 4

US-08-483-636-73

Sequence 73, Application US/08483636

Patent No. 5914110

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.

APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

TITLE OF INVENTION: Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P.O. Box 1539 / UM2220

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-483-636-73

Query Match 70.4%; Score 38; DB 2; Length 111;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QUCNEDPPT 9
DB 93 QOSNEDPPT 101

RESULT 5
US-08-483-632-73
Sequence 73, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-483-632-73

Query Match 70.4%; Score 38; DB 2; Length 111;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QUCNEDPPT 9
DB 93 QOSNEDPPT 101

RESULT 6
US-08-137-117D-33
Sequence 33, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-33

Query Match 70.4%; Score 38; DB 1; Length 131;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9
DB 113 QOSNEDPPT 121

US-08-436-717-33
Sequence 33, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Maayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436, 717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137, 117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: MEGNER, Harold C.
REGISTRATION/DOCKET NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-33

Query Match 70.4%; Score 38; DB 2; Length 131;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9
DB 113 QOSNEDPPT 121

RESULT 8
US-08-621-751A-10
Sequence 10, Application US/08621751A
Patent No. 5882644
GENERAL INFORMATION:
APPLICANT: Chang, Chung N.
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Martin, Ulrich
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621, 751A
FILING DATE: 22-MAR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 321152000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141 MRSN FOERS SFO
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-621-751A-10

Query Match 70.4%; Score 38; DB 2; Length 131;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9
DB 113 QOSNEDPPT 121

RESULT 9
US-08-621-751A-14
Sequence 14, Application US/08621751A
Patent No. 5882644
GENERAL INFORMATION:
APPLICANT: Chang, Chung N.
APPLICANT: Landolfi, Nicholas F.

APPLICANT: Martin, Ulrich
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE
TITLE OF INVENTION: PLATELET-DRIVEN GROWTH FACTOR RECEPTOR BETA RECEPTOR AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,751A
FILING DATE: 22-MAR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 321152000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141 MRSN FOERS SFO
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-621-751A-14

Query Match 70.4%; Score 38; DB 2; Length 131;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLCNEDPPT 9
Db 113 QOSNEDPPT 121

RESULT 10
US-08-636-58
Sequence 58, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-636-58

Query Match 70.4%; Score 38; DB 2; Length 131;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLCNEDPPT 9
Db 112 QOSNEDPPT 120

RESULT 11
US-08-483-632-58
Sequence 58, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-632-58

Query Match 70.4%; Score 38; DB 2; Length 131;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDDPT 9
Db 112 QOSNEDDPT 120

SULT 12
US-08-483-636-2
Sequence 2, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Groves, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
OPERATING SYSTEM: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-636-2

Query Match 70.4%; Score 38; DB 2; Length 132;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDDPT 9
Db 113 QOSNEDDPT 121

RESULT 13
US-08-483-632-2
Sequence 2, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Groves, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
OPERATING SYSTEM: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-632-2

Query Match 70.4%; Score 38; DB 2; Length 132;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDDPT 9
Db 113 QOSNEDDPT 121

RESULT 14
US-08-465-380-4

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; Sequence 4, Application US/08465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemaens, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 955-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; 8-465-380-4

Query Match          66.7% Score 36; DB 2; Length 77;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 CNEDEP 8
      |||:|
DB      25 CNEEPP 30

RESULT 15
US-08-465-380-40
; Sequence 40, Application US/08465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemaens, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-465-380-40

Query Match          66.7% Score 36; DB 2; Length 77;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 CNEDEP 8
      |||:|
DB      25 CNEEPP 30
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Job time : 14.05 secs

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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:42:07 ; Search time 18 Seconds
(without alignments)
72.956 Million cell updates/sec

Title: US-09-759-112a-36

Perfect score: 54
Sequence: 1 OLCNDDPT 9

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Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	9	11 US-09-759-112a-36	Sequence 36, Appl
2	54	100.0	110	11 US-09-759-112a-24	Sequence 24, Appl
3	41	75.9	407	14 US-10-085-108-26	Sequence 26, Appl
4	39	72.2	399	9 US-09-729-674-94	Sequence 94, Appl
5	38	70.4	9	10 US-09-879-461-20	Sequence 20, Appl
6	38	70.4	112	10 US-09-144-886-80	Sequence 80, Appl
7	38	70.4	131	10 US-09-879-461-58	Sequence 58, Appl
8	38	70.4	132	10 US-09-879-461-2	Sequence 2, Appl
9	38	70.4	272	15 US-10-207-655-112	Sequence 112, Appl
10	36	66.7	77	11 US-09-498-272-4	Sequence 4, Appl
11	36	66.7	77	11 US-09-498-272-40	Sequence 40, Appl
12	36	66.7	81	11 US-09-498-272-7	Sequence 7, Appl
13	36	66.7	100	11 US-09-498-272-20	Sequence 20, Appl
14	36	66.7	141	11 US-09-764-891-3695	Sequence 3695, Ap
15	36	66.7	181	15 US-10-156-761-7554	Sequence 7554, Ap

16	35	64.8	356	12 US-10-017-161-1738	Sequence 1738, Ap
17	35	64.8	402	10 US-09-738-626-5344	Sequence 5344, Ap
18	35	64.8	491	11 US-09-999-2208-4	Sequence 4, Appl
19	35	64.8	731	10 US-09-981-423-2	Sequence 2, Appl
20	35	64.8	1420	10 US-09-801-368-356	Sequence 356, App
21	34	63.0	377	9 US-09-849-031A-3	Sequence 3, Appl
22	34	63.0	377	9 US-09-849-562A-3	Sequence 3, Appl
23	34	63.0	377	12 US-10-329-068-3	Sequence 3, Appl
24	34	63.0	543	10 US-09-925-300-1700	Sequence 1700, Ap
25	33	61.1	9	10 US-09-879-461-28	Sequence 28, Appl
26	33	61.1	10	11 US-09-563-222-34	Sequence 34, Appl
27	33	61.1	70	14 US-10-068-347-12	Sequence 12, Appl
28	33	61.1	80	11 US-09-764-891-3444	Sequence 3444, Ap
29	33	61.1	91	9 US-09-864-761-48847	Sequence 48847, A
30	33	61.1	112	12 US-10-160-506-81	Sequence 81, Appl
31	33	61.1	116	9 US-09-764-869-689	Sequence 689, App
32	33	61.1	116	15 US-10-091-504-689	Sequence 689, App
33	33	61.1	131	10 US-09-879-461-14	Sequence 14, Appl
34	33	61.1	144	9 US-09-784-810A-8	Sequence 8, Appl
35	33	61.1	148	9 US-09-867-550-544	Sequence 544, App
36	33	61.1	176	12 US-10-259-165-86	Sequence 86, Appl
37	33	61.1	176	12 US-10-259-165-346	Sequence 346, App
38	33	61.1	176	14 US-10-078-929-86	Sequence 86, Appl
39	33	61.1	196	15 US-10-189-346-1	Sequence 1, Appl
40	33	61.1	200	15 US-09-227-488-1	Sequence 4, Appl
41	33	61.1	200	15 US-10-189-346-31	Sequence 31, Appl
42	33	61.1	200	15 US-10-189-346-32	Sequence 32, Appl
43	33	61.1	201	15 US-10-189-346-29	Sequence 29, Appl
44	33	61.1	201	15 US-10-189-346-30	Sequence 30, Appl
45	33	61.1	280	12 US-10-259-165-174	Sequence 174, App

ALIGNMENTS

RESULT 1
US-09-759-112a-36
; Sequence 36, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1E7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
US-09-759-112a-36

Query Match 100.0%; Score 54; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 OLCNDDPT 9
Db 1 OLCNDDPT 9

RESULT 2
US-09-759-112a-24
; Sequence 24, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT

TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 110
TYPE: PRT
ORGANISM: mouse
US-09-759-112a-24

Query Match 100.0%; Score 54; DB 11; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNDDPPT 9
:|||||
92 QLCNDDPPT 100

RESULT 3
US-10-085-108-26
Sequence 26, Application US/10085108
Publication No. US20020176865A1
GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie; BOON-PALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
FOR
TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C
MAGE-B FAMILIES AND USES THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Publight & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/085,108
FILING DATE: 01-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/501,104
FILING DATE: 09-Feb-2000
APPLICATION NUMBER: 09/468,433
FILING DATE: December 17, 1999
APPLICATION NUMBER: 09/066,281
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 407
TYPE: amino acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-085-108-26

Query Match 75.9%; Score 41; DB 14; Length 407;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLCNDDPPT 8
:|||||
Db 346 QVCNSDDPPT 353

RESULT 4
US-09-729-674-94
Sequence 94, Application US/09729674
Patent No. US20010039335A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steindinger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 94
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
US-09-729-674-94

Query Match 72.2%; Score 39; DB 9; Length 399;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCNDDPPT 9
:|||||
Db 279 MCDNDDPPT 286

RESULT 5
US-09-879-461-20
Sequence 20, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
NFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-879-461-20

Query Match 70.4%; Score 38; DB 10; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.8e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9
| |||||
Db 1 QOSNEDPPT 9

RESULT 6
US-09-144-886-80
Sequence 80, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amerdoffer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 80
LENGTH: 112
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
OTHER INFORMATION: 1B6 region VL epitope 1
US-09-144-886-80

Query Match 70.4%; Score 38; DB 10; Length 112;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9
| |||||
Db 93 QOSNEDPPT 101

RESULT 7
US-09-879-461-58
Sequence 58, Application US/09879461
Publication No. US20020193575A1

GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-879-461-58

Query Match 70.4%; Score 38; DB 10; Length 131;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9
| |||||
Db 112 QOSNEDPPT 120

RESULT 8
US-09-879-461-2
Sequence 2, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2

Query Match 70.4%; Score 38; DB 10; Length 132;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEDPP 9
| | | | |
| | | | |
Db 113 QCSNEDPP 121

RESULT 9
US-10-207-655-172
Sequence 172, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
FILE REFERENCE: 390069,401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 172
LENGTH: 272
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-172

Query Match 70.4%; Score 38; DB 15; Length 272;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNEDPP 8
| | | | |
| | | | |
Db 22 ELCDDDPP 29

RESULT 10
US-09-498-272-4
Sequence 4, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlaeuk, George Phillip

Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Ganssemans, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-498-272-4

Query Match 66.7%; Score 36; DB 11; Length 77;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPP 8
| | | | |
| | | | |
Db 25 CNEDEPP 30

RESULT 11
US-09-498-272-40
Sequence 40, Application US/09498272

Publication No. US20030113890A1
 GENERAL INFORMATION:
 APPLICANT: Vlasuk, George Phillip
 Stanssens, Patrick Eric Hugo
 Messens, Joris Hilda Lieven
 Lauwereys, Marc Josef
 Laroche, Yves Rene
 Jespers, Laurent Stephane
 Ganssemans, Yannick Georges Jozef
 Moyle, Matthew
 Bergum, Peter W.
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 INHIBITORS AND ANTICOAGULANT
 PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/498,272
 FILING DATE: 04-Feb-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13231
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 216/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 77 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Ancylostoma caninum
 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
 US-09-498-272-40
 Query Match 66.7%; Score 36; DB 11; Length 77;
 Best Local Similarity 83.3%; Pred. No. 44;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 US-09-498-272-7
 Sequence 7, Application US/09498272
 Publication No. US20030113890A1
 GENERAL INFORMATION:
 APPLICANT: Vlasuk, George Phillip
 Stanssens, Patrick Eric Hugo
 Messens, Joris Hilda Lieven
 Lauwereys, Marc Josef
 Laroche, Yves Rene
 Jespers, Laurent Stephane
 Ganssemans, Yannick Georges Jozef
 Moyle, Matthew
 Bergum, Peter W.
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 INHIBITORS AND ANTICOAGULANT
 PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/498,272
 FILING DATE: 04-Feb-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13231
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 216/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 81 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Ancylostoma caninum
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-498-272-7
 Query Match 66.7%; Score 36; DB 11; Length 81;
 Best Local Similarity 83.3%; Pred. No. 46;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 CNEEPP 34

RESULT 13

US-09-498-272-20
Sequence 20, Application US/09498272
Publication No. US20030113890A1

GENERAL INFORMATION:

APPLICANT: Vlaauk, George Phillip

Stanssens, Patrick Eric Hugo

Messens, Joris Hilda Lieven

Lauwereys, Marc Josef

Laroche, Yves Rene

Jespers, Laurent Stephane

Gansemans, Yannick Georges Jozef

Moyle, Matthew

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

INHIBITORS AND ANTICOAGULANT

PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Filth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498.272

FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 100 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Ancylostoma caninum

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-498-272-20

Query Match 66.7%; Score 36; DB 11; Length 100;

Best Local Similarity 83.3%; Pred. No. 57;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEEPP 8
Db 48 CNEEPP 53

RESULT 14

US-09-764-891-3695
Sequence 3695, Application US/09764891
Publication No. US20030077808A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006

CURRENT APPLICATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 10231

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3695

LENGTH: 141

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (78)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (90)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (102)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-891-3695

Query Match 66.7%; Score 36; DB 11; Length 141;

Best Local Similarity 66.7%; Pred. No. 79;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLCNEEPP 9

RESULT 15

US-10-156-761-7554
Sequence 7554, Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 7554

LENGTH: 181

TYPE: PRT

ORGANISM: Streptomyces avermitilis

US-10-156-761-7554

Query Match 66.7%; Score 36; DB 15; Length 181;

Best Local Similarity 75.0%; Pred. No. 1e+02;

Matches	6;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2	LCNDDPPT	9						
Db	67	LCQBGSPPT	74						

Search completed: September 10, 2003, 17:50:28
Job time : 19 secs

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PT region of an anti-idiotypic antibody that binds to human or primate
PT anti- human immunodeficiency virus (HIV) antibodies, for use in
PT vaccines against HIV -

XX Claim 4; Page 27; 27pp; English.

CC The present invention relates to coding sequences of the murine 1F7
CC anti-idiotypic antibody complementarity-determining region (CDR) or
CC framework-determining region (FR). The antibody binds to human or primate
CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the
CC treatment of HIV infection. The present sequence is a region of the 1F7
CC light chain.

XX Sequence 9 AA;

Query Match 100.0%; Score 54; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QLCNEDPPT 9
1 QLCNEDPPT 9

RESULT 2
AAV91016 standard; protein; 28 AA.

AAV91016;

05-SEP-2000 (first entry)

1F7 antibody variable light chain L3 amino acid sequence SEQ ID NO:7.

1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
AIDS; anti-HIV; human immunodeficiency virus; detection;
acquired immunodeficiency syndrome.

Mus sp.

US6057421-A.

02-MAY-2000.

03-DEC-1997; 97US-0984277.

30-NOV-1994; 94US-0351193.

(IMMP-) IMPHERON INC.

Muller S, Kohler H;

WPI; 2000-338622/29.

Variable heavy and light chain regions of murine monoclonal antibody
1F7, useful for treating HIV infection and AIDS -

Claim 1; Fig 8; 45pp; English.

The present invention describes the variable heavy and light chain
regions (1) of murine monoclonal antibody (mAb) 1F7. AAV91014 to
AAV91016 represent specifically claimed amino acid sequences of the
variable light chain, and AAV91017 to AAV91019 represent specifically
claimed amino acid sequence of the variable heavy chain. The antibodies
are used for treatment of HIV (human immunodeficiency virus) infection
and AIDS (acquired immunodeficiency syndrome). They are also used for
detecting HIV in serum and for stimulating HIV antigen related and
committed B cells to produce broadly reactive and neutralising antibodies
by clonotypic stimulation.

Sequence 28 AA;

Query Match 100.0%; Score 54; DB 21; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9
1 QLCNEDPPT 18

RESULT 3
AAO18536 standard; protein; 110 AA.

AAO18536;

11-OCT-2002 (first entry)

Murine Mab 1F7 light chain.

Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
complementarity determining region; framework-determining region;
FR; heavy chain; light chain; HIV infection.

Mus sp.

WO200255668-A2.

18-JUL-2002.

11-JAN-2002; 2002MO-US00927.

11-JAN-2001; 2001US-0759112.

(IMMP-) IMPHERON INC.

Muller S, Kohler H;

WPI; 2002-590668/63.

N-PSDB; AAL48661.

New polynucleotide encoding a complementarity- or framework-determining
region of an anti-idiotypic antibody that binds to human or primate
anti- human immunodeficiency virus (HIV) antibodies, for use in
vaccines against HIV -

Claim 9; Page 23-24; 27pp; English.

The present invention relates to coding sequences of the murine 1F7
anti-idiotypic antibody complementarity-determining region (CDR) or
framework-determining region (FR). The antibody binds to human or primate
anti-human immunodeficiency virus (HIV) antibodies and can be used in the
treatment of HIV infection. The present sequence is the 1F7 light chain.

Sequence 110 AA;

Query Match 100.0%; Score 54; DB 23; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNEDPPT 9
1 QLCNEDPPT 100

RESULT 4
ABU08934 standard; protein; 407 AA.

ABU08934;

05-JUN-2003 (first entry)

Human tumour rejection antigen precursor, MAGE-B6.

KW TRAP: tumour rejection antigen precursor; cytolytic T-cell; CTL;
 KW tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor;
 KW head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma;
 KW cutaneous melanoma; nonsmall cell lung cancer; MAGS-B6; human.

OS Homo sapiens.

XX US2002176865-A1.

XX 28-NOV-2002.

XX 01-MAR-2002; 2002US-0085108.

XX 09-FEB-2000; 2000US-0501104.

XX 25-APR-1997; 97US-0845528.

XX 24-APR-1998; 98US-0066281.

XX 17-DEC-1999; 99US-0468433.

XX (LUCAS/) LUCAS S.

XX (BOON/) BOON-FALLEUR T.

XX Lucas S, Boon-Falleur T;

XX WPI: 2003-328468/31.

XX N-PSDB; ABX95008.

XX Novel isolated nucleic acid encoding tumor rejection antigen precursor

XX MAGS-C3, MAGS-B5, or MAGS-B6, useful as diagnostic probes to determine

XX presence of abnormal e.g., tumor cells expressing MAGS-C1, MAGS-B5 or

XX MAGS-B6

XX Example 13; Fig 10; 59pp; English.

XX The invention relates to an isolated nucleic acid molecule which encodes

XX a tumour rejection antigen precursor (TRAP) having an amino acid sequence

XX of a TRAP encoded by a fully defined MAGS-C3, MAGS-B5, or MAGS-B6

XX polynucleotide sequence. Also disclosed is a method which is useful for

XX determining presence of cytolytic T-cells specific for complexes of human

XX leukocyte antigen (HLA) and a peptide derived from the nucleic acid in a

XX cytotoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is

XX useful as a diagnostic probe to determine the presence of abnormal

XX (tumour) cells such as seminoma, bladder transitional-cell carcinoma,

XX head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma,

XX cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express

XX MAGS-C1, MAGS-B5 or MAGS-B6. The nucleic acid is useful for diagnosing a

XX disorder characterised by expression of MAGS-C1, MAGS-B5 or MAGS-B6 TRAPs

XX or tumour rejection antigens (TRAPs). The present sequence represents the

XX amino acid sequence of the human tumour rejection antigen precursor,

XX MAGS-B6.

XX Sequence 407 AA;

XX Query Match 75.9%; Score 41; DB 24; Length 407;

XX Best Local Similarity 75.0%; Pred. No. 43;

XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX 1 QLCNEDPP 8

XX 346 QVCNSDDP 353

XX Db

XX RESULT 5

XX ABG23972

XX ID ABG23972 standard; Protein; 54 AA.

XX ABG23972;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #23963.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB; AAS88159.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity

XX Claim 20; SEQ ID NO 54331; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

XX polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX and gene mapping, and in recombinant production of (II). The

XX polynucleotides are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes. (I) is useful in gene therapy techniques

XX to restore normal activity of (II) or to treat disease states involving

XX (II). (II) is useful for generating antibodies against it, detecting or

XX quantitating a polypeptide in tissue, as molecular weight markers and as

XX a food supplement. (II) and its binding partners are useful in medical

XX imaging of sites expressing (II). (I) and (II) are useful for treating

XX disorders involving aberrant protein expression or biological activity.

XX The polypeptide and polynucleotide sequences have applications in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits to assess biodiversity

XX and to produce other types of data and products dependent on DNA and

XX amino acid sequences. ABG00010-ABG30377 represent novel human

XX CC diagnostic amino acid sequences of the invention.

XX Note: The sequence data for this patent did not appear in the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 54 AA;

XX Query Match 72.2%; Score 39; DB 22; Length 54;

XX Best Local Similarity 75.0%; Pred. No. 14;

XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX 2 LCNEDPPT 9

XX 7 LCEKXDPT 14

XX Db

XX RESULT 6

XX ABP09856

XX ID ABP09856 standard; Protein; 54 AA.

XX ABP09856;

XX 24-JUN-2002 (first entry)

XX Human ORFX protein sequence SEQ ID NO:19694.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

XX degenerative disorder; osteoarthritis; neurodegenerative disorder;

XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 OS Homo sapiens.
 PN WO200192523-A2.
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US10836.
 XX
 PR 30-MAY-2000; 2000US-206132P.
 PR 29-AUG-2000; 2000US-228716P.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Shimkete RA, Leach MD;
 PI WPI; 2002-106308/14.
 PI N-Psdb; ABN25608.
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders -
 PS Disclosure; SEQ ID 19694; 1037pp; English.
 XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-1191 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 54 AA;
 XX
 QY Query Match 72.2%; Score 39; DB 23; Length 54;
 DB Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QLCNEDPPT 9
 |||: |||
 DB 39 QLCQDSPPT 47
 |||: |||
 RESULT 7
 ID ABG20915 standard; Protein; 70 AA.
 XX
 AC ABG20915;
 DT 13-FEB-2002 (first entry)

XX
 DE Novel human diagnostic protein #20906.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 PI N-Psdb; AAS85102.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20; SEQ ID No 51274; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostic, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG3037 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 70 AA;
 XX
 QY Query Match 72.2%; Score 39; DB 22; Length 70;
 DB Best Local Similarity 75.0%; Pred. No. 18;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LCNEDPPT 9
 |||: |||
 DB 19 LCKEDPPT 26
 |||: |||
 RESULT 8
 ID ABG15042 standard; Protein; 73 AA.
 XX
 AC ABG15042;
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #15033.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 XX N-PSDB; AAS79229.
 PT -New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20; SEQ ID No 45401; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 73 AA;
 QY Query Match 72.2%; Score 39; DB 22; Length 73;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LCNEPPT 9
 Db 19 LCEKDPPT 26
 RESULT 9
 ABG18578
 ID ABG18578 standard; Protein; 73 AA.
 XX
 AC ABG18578;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #18569.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 XX N-PSDB; AAS82765.
 PT -New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20; SEQ ID No 48937; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 73 AA;
 QY Query Match 72.2%; Score 39; DB 22; Length 73;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LCNEPPT 9
 Db 19 LCEKDPPT 26
 RESULT 10
 ABG19791
 ID ABG19791 standard; Protein; 74 AA.
 XX
 AC ABG19791;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #19782.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.
XX WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX PF 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX DR N-PSDB; AAS68297.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
PS Claim 20; SEQ ID No 50150; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 74 AA;
XX
XX Query Match 72.2%; Score 39; DB 22; Length 74;
XX Best Local Similarity 75.0%; Pred. No. 19;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPPT 9
DB 19 LCEKDPPT 26

RESULT 11
ABG04110
ID ABG04110 standard; Protein; 77 AA.
XX
XX
AC ABG04110;
XX
DT 13-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #4101.
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX

PN WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX PF 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX DR N-PSDB; AAS68297.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
PS Claim 20; SEQ ID No 34463; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 77 AA;
XX
XX Query Match 72.2%; Score 39; DB 22; Length 77;
XX Best Local Similarity 75.0%; Pred. No. 20;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPPT 9
DB 24 LCEKDPPT 31

RESULT 12
ABG23982
ID ABG23982 standard; Protein; 78 AA.
XX
XX
AC ABG23982;
XX
DT 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #23973.
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX

PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
PF 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS88169.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

Claim 20; SEQ ID No 54341; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX

Sequence 78 AA;

Query Match 72.2%; Score 39; DB 22; Length 78;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 LCNEDEPT 9
||:||||
Db 23 LCEKDPPT 30

RESULT 13

ABG25273
ID ABG25273 standard; Protein; 99 AA.
XX

AC ABG25273;
XX

DT 18-FEB-2002 (first entry)
XX

DE Novel human diagnostic protein #25264.
XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX

OS Homo sapiens.
XX

PN WO200175067-A2.
XX

PD 11-OCT-2001.
XX

PF 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS89460.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

Claim 20; SEQ ID No 55632; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX

Sequence 99 AA;

Query Match 72.2%; Score 39; DB 22; Length 99;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPT 9
||:||||
Db 19 LCEKDPPT 26

RESULT 14

ABG18624
ID ABG18624 standard; Protein; 118 AA.
XX

AC ABG18624;
XX

DT 18-FEB-2002 (first entry)
XX

DE Novel human diagnostic protein #18615.
XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX

OS Homo sapiens.
XX

PN WO200175067-A2.
XX

PD 11-OCT-2001.
XX

PF 30-MAR-2001; 2001WO-US08631.
XX

PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 XX N-PSDB; AAS82811.
 DR
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 48983; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences..
 CC
 SQ Sequence 118 AA;
 Query Match 72.2%; Score 39; DB 22; Length 118;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 LCNEDEPPT 9
 Db 65 LCNEDEPPT 72
 ID AAY74157 standard; Protein; 284 AA.
 AC AAY74157;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Human prostate tumor EST fragment derived protein #344.
 XX
 KM Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
 XX treatment.
 OS Homo sapiens.
 XX
 PN DE19820190-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 28-APR-1998; 98DE-1020190.
 XX
 BR 28-APR-1998; 98DE-1020190.
 XX

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX WPI; 1999-621386/54.
 DR N-PSDB; AA252971.
 XX
 PT New human nucleic acid sequences from pancreatic tumors, and related
 PT proteins -
 XX
 PS Claim 23; Page 452; 502pp; German.
 XX
 CC This invention describes novel polypeptides and their encoding nucleic
 CC acids derived from human pancreatic tumor tissue which have cytostatic
 CC activity. The sequences are also useful in producing pharmaceutical
 CC compositions for treatment of pancreatic tumors. AAY73814-Y74252
 CC represent protein fragments encoded by the human pancreatic tumor cDNA
 CC library derived expressed sequence tag (EST) sequences represented in
 CC AA252858-253014.
 CC
 SQ Sequence 284 AA;
 Query Match 72.2%; Score 39; DB 20; Length 284;
 Best Local Similarity 62.5%; Pred. No. 68;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 LCNEDEPPT 9
 Db 164 MCDDDEPPT 171
 Search completed: September 10, 2003, 17:40:20
 Job time : 32.95 secs

DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE 2-oxoglutarate dehydrogenase e1 component.
 GN SPBC3H7.03C.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Lyne M., Rajandream M.A., Barrell B.G., Jimeenez Martinez J;
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031261; CAA20299.1; -;
 DR GeneDB Spombe; SPBC3H7.03C; -;
 DR InterPro: IPR001017; Dehydrogenase_E1.
 DR InterPro: IPR005475; Transketolase_CR.
 DR Pfam; PF00676; E1_dehydrog; 1.
 DR Pfam; PF02779; transket_pyr; 1.
 DR TIGRFAMs; TIGR00239; 2oxo_ch_E1; 1.
 SEQUENCE 1009 AA; 114163 MW; 4CB2598CE2B5E6AB CRC64;

Query Match 77.8%; Score 42; DB 3; Length 1009;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLCNEDP 7
 Db 792 QLCNEDP 798

RESULT 3
 Q88N7X4 PRELIMINARY; PRT; 407 AA.
 AC Q88N7X4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE Hypothetical protein FJ40242.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
 RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isegai T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK097361; BAC05102.1; -;
 DR InterPro: IPR02190; MAGE.
 DR Pfam; PF01454; MAGE; 2.
 DR PROSITE; PS00838; MAGE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 407 AA; 44091 MW; D674F426131244C0 CRC64;

Query Match 75.9%; Score 41; DB 4; Length 407;
 Best Local Similarity 75.0%; Pred. No. 7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLCNEDP 8
 Db 346 QVCNSDPP 353

RESULT 4
 Q88N7X4 PRELIMINARY; PRT; 339 AA.
 ID Q88N7X4

AC Q88X24;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE Conserved hypothetical protein.
 GN LB063.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE011595; AAN51622.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 339 AA; 39035 MW; A7F815C3EA23CDD9 CRC64;

Query Match 74.1%; Score 40; DB 16; Length 339;
 Best Local Similarity 85.7%; Pred. No. 9.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CNEDEPT 9
 Db 152 CNEDEPT 158

RESULT 5
 Q88V1 PRELIMINARY; PRT; 1051 AA.
 AC Q88V1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE Putative transcription factor LUZP.
 GN LUZP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96411647; PubMed=8812416;
 RA Sun D.S., Chang A.C., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Chang N.C.;
 RT "Identification, molecular characterization, and chromosomal
 localization of the cDNA encoding a novel leucine zipper motif-
 containing protein."
 RL Genomics 36:54-62(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Sun D.S., Chang A.C., Lai S.H., Hsu C.Y., Chang N.C.;
 RT "Expression of a novel leucine zipper motif-containing protein (LUZP)
 in brain."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF181259; AAG02142.1; -;
 DR HSSP; P04268; 1IC2.
 SQ SEQUENCE 1051 AA; 117175 MW; FE1F3D7100326843 CRC64;

Query Match 74.1%; Score 40; DB 11; Length 1051;
 Best Local Similarity 85.7%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CNEDEPT 9
 Db 933 CSEDDPT 939

RESULT 6
 Q88A47 PRELIMINARY; PRT; 1068 AA.
 ID Q88A47


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AC Q8R4U7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE leucine zipper motif-containing protein.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=96411647; PubMed=8812416;
RA Sun D.S., Chang A.C., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Chang N.C.;
RT "Restricted Expression of LUPZ in Neural Lineage Cells: A Study in
RT Embryonic Stem Cells.";
RL J. Biomed. Sci. 8:504-511(2001).
DR EMBL; AF362727; AACM00269.1; -.
DR HSSP; P04268; 1IC2.
SQ SEQUENCE 1068 AA; 119404 MW; 148153E01C1643C3 CRC64;

Query Match
Best Local Similarity 74.1%; Score 40; DB 11; Length 1068;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPPT 9
DB 928 CSEDPPT 934

RESULT 7
Q8LSX2 PRELIMINARY; PRT; 267 AA.
ID Q8LSX2;
AC Q8LSX2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
OS Chaamecypris pisifera.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
OC Chaamecypris.
OX NCBI_TaxID=99808;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsunura Y., Yoshimaru H., Tachida H.;
RA "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
DR EMBL; AB076600; BAB91464.1; -.
DR InterPro; IPR001005; MYB_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 267 AA; 28342 MW; F0FE23272A29299CA CRC64;

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Query Match
Best Local Similarity 72.2%; Score 39; DB 10; Length 267;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPPT 9
DB 146 LCSDPPT 153

RESULT 8
Q8LSY0 PRELIMINARY; PRT; 268 AA.
ID Q8LSY0;
AC Q8LSY0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
OS Taxodium distichum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Taxodium.
OX NCBI_TaxID=28982;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsunura Y., Yoshimaru H., Tachida H.;
RA "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
DR EMBL; AB076592; BAB91456.1; -.
DR InterPro; IPR001005; MYB_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 268 AA; 28545 MW; 0A17853E70424FA5 CRC64;

Query Match
Best Local Similarity 72.2%; Score 39; DB 10; Length 268;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPPT 9
DB 146 LCSDPPT 153

RESULT 9
Q8LSX8 PRELIMINARY; PRT; 268 AA.
ID Q8LSX8;
AC Q8LSX8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
OS Sequoia sempervirens (California redwood).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Sequoia.
OX NCBI_TaxID=28980;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsunura Y., Yoshimaru H., Tachida H.;
RA "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
DR EMBL; AB076594; BAB91458.1; -.

```

DR InterPro; IPR001005; Myb DNA binding.
DR Pfam; PF00249; myb DNA-binding; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 268 AA; 28727 MW; 9BCF7F872A24031B CRC64;

Query Match 72.2%; Score 39; DB 10; Length 268;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
||:||||
Db 146 LCSSDPPT 153

RESULT 10

OS SY1 PRELIMINARY; PRT; 268 AA.
AC OBLSY1;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.

OS Glyptostrobus lineatus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
OC Glyptostrobus.
OX NCBI_TaxID=28978;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21959336; PubMed=11961107;
RA Kusum J., Tsunura Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of Conifer Trees."
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

DR EMBL; AB076591; BAB91455.1; -
DR InterPro; IPR001005; Myb DNA-binding.
DR Pfam; PF00249; myb DNA-binding; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 268 AA; 28597 MW; D196D2C3126A5ECF CRC64;

Query Match 72.2%; Score 39; DB 10; Length 268;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
||:||||
Db 146 LCSSDPPT 153

RESULT 11

OS SY1 PRELIMINARY; PRT; 285 AA.
AC OBLSY1;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.

OS Thruja standishii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Thruja.
OX NCBI_TaxID=89194;

RN [1]
SQ SEQUENCE FROM N.A.

RX MEDLINE=21959336; PubMed=11961107;
RA Kusum J., Tsunura Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of Conifer Trees."
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

DR EMBL; AB076597; BAB91461.1; -
DR InterPro; IPR001005; Myb DNA-binding.
DR Pfam; PF00249; myb DNA-binding; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 285 AA; 30436 MW; CCDAB13A5A052725 CRC64;

Query Match 72.2%; Score 39; DB 10; Length 285;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
||:||||
Db 163 LCSSDPPT 170

RESULT 12

OS SY1 PRELIMINARY; PRT; 285 AA.
AC OBLSY1;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.

OS Chaamecypris pisifera.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
OC Chaamecypris.
OX NCBI_TaxID=99808;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21959336; PubMed=11961107;
RA Kusum J., Tsunura Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of Conifer Trees."
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.

DR EMBL; AB076595; BAB91459.1; -
DR InterPro; IPR001005; Myb DNA-binding.
DR Pfam; PF00249; myb DNA-binding; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 285 AA; 30272 MW; D1039F7FF610ADDF CRC64;

Query Match 72.2%; Score 39; DB 10; Length 285;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
||:||||
Db 163 LCSSDPPT 170

RESULT 13

OS SY1 PRELIMINARY; PRT; 285 AA.
AC OBLSY1;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.

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AC 08LSX6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.
OS Thujopsis dolabrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Thujopsis.
OX NCBI_TaxID=13727;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsunuma Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB076596; BAB91460.1; -
InterPro: IPR001005; Myb DNA binding.
Pfam: PF00249; myb DNA-binding; 1.
DR SMART: SM00717; SANT; 1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON TER 1
SQ SEQUENCE 285 AA; 30429 MW; F875D9C8EF2402F3 CRC64;

Query Match 72.2%; Score 39; DB 10; Length 285;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
DB 163 LCSSDPPT 170

RESULT 14
08LSX3 PRELIMINARY; PRT; 285 AA.
AC 08LSX3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.
OS Chamaecyparis obtusa (Japanese Cypress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
OC Chamaecyparis.
OX NCBI_TaxID=13415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsunuma Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB076599; BAB91463.1; -
InterPro: IPR001005; Myb DNA binding.
Pfam: PF00249; myb DNA-binding; 1.
DR SMART: SM00717; SANT; 1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON TER 1
SQ SEQUENCE 285 AA; 30290 MW; 876C964CA03A7108 CRC64;

Query Match 72.2%; Score 39; DB 10; Length 285;
Best Local Similarity 75.0%; Pred. No. 12;
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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
DB 163 LCSSDPPT 170
```

```
RESULT 15
08LSX4 PRELIMINARY; PRT; 286 AA.
AC 08LSX4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myb transcription factor (Fragment).
GN MYB.
OS Juniperus rigida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
OX NCBI_TaxID=99809;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959336; PubMed=11961107;
RA Kusumi J., Tsunuma Y., Yoshimaru H., Tachida H.;
RT "Molecular Evolution of Nuclear Genes in Cupressaceae, a Group of
RT Conifer Trees.";
RL Mol. Biol. Evol. 19:736-747(2002).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB076598; BAB91462.1; -
InterPro: IPR001005; Myb DNA binding.
Pfam: PF00249; myb DNA-binding; 1.
DR SMART: SM00717; SANT; 1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON TER 1
SQ SEQUENCE 286 AA; 30647 MW; 7582049879D40A22 CRC64;
```

```
Query Match 72.2%; Score 39; DB 10; Length 286;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
DB 164 LCSSDPPT 171
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Search completed: September 10, 2003, 17:42:05
Job time : 27.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:34:47 ; Search time 9 Seconds
(without alignments)
47.027 Million cell updates/sec

Title: US-09-759-112a-36
Perfect score: 54
Sequence: 1 QLCNEDPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	72.2	399	TE21_HUMAN	Q9Nyb0 homo sapien
2	38	70.4	272	IL2A_HUMAN	P01589 homo sapien
3	37	68.5	701	YAB5_SCHPO	009807 schizosacch
4	37	68.5	1002	ODO1_HUMAN	002218 homo sapien
5	36	66.7	268	IL2A_CANFA	062802 canis fami
6	36	66.7	275	IL2A_FELCA	P41590 felis silve
7	36	66.7	359	TPS8_CABEL	Q20351 caenorhabi
8	36	66.7	385	TPST_DROME	Q9Vyb7 drosophila
9	35	64.8	380	TPSA_CABEL	077081 caenorhabi
10	35	64.8	393	TE21_MOUSE	Q91V18 mus musculu
11	35	64.8	491	KCS3_RABIT	Q9C173 oryctolagus
12	35	64.8	491	KCS3_RAT	Q88759 rattus norv
13	35	64.8	598	GATE_THERVO	Q97919 rattus norv
14	35	64.8	692	DPR2_YEAST	P24482 saccharomyc
15	35	64.8	1420	SRB9_YEAST	P38931 saccharomyc
16	34	63.0	275	IL2A_BOVIN	P12342 bos taurus
17	34	63.0	275	IL2A_SHEEP	P26898 ovie aries
18	34	63.0	322	SSAO_SALTY	F74860 salmonella
19	34	63.0	340	TFZB_SCHPO	013749 schizosacch
20	34	63.0	376	TPS2_MOUSE	088856 mus musculu
21	34	63.0	377	TPS2_HUMAN	067074 homo sapien
22	34	63.0	621	GP63_LEIGU	000669 leishmania
23	34	63.0	860	CHIZ_COCPO	P54197 coccidioidi
24	34	63.0	1003	TP3A_MOUSE	Q70157 mus musculu
25	34	63.0	1928	LPH_RAT	Q02491 rattus norv
26	33	61.1	168	PR1A_TOBAC	P08289 nicotiana t
27	33	61.1	168	PR1B_TOBAC	P07053 nicotiana t
28	33	61.1	168	PR1C_TOBAC	P09042 nicotiana t
29	33	61.1	173	PRL1_MEDPR	Q40374 medicago tr
30	33	61.1	175	PRL1_LYCES	Q08697 lycopersico
31	33	61.1	177	PRB1_TOBAC	P16760 nicotiana t
32	33	61.1	201	RHL1_PSEAE	P54291 pseudomonas
33	33	61.1	210	INSR_MACMU	Q28516 macaca mula

34	33	61.1	211	1	NDK5_MOUSE	Q99mh5 mus musculu
35	33	61.1	256	1	TPS1_BRARE	Q99tes brachydanto
36	33	61.1	324	1	SG10_CABEL	P45668 caenorhabi
37	33	61.1	370	1	TPS1_HUMAN	060507 homo sapien
38	33	61.1	370	1	TPS1_MOUSE	070281 mus musculu
39	33	61.1	611	1	GHR_COLLI	Q90375 columba liv
40	33	61.1	731	1	HRPM_PSEESY	P20401 pseudomonas
41	33	61.1	816	1	NPA2_MOUSE	P97460 mus musculu
42	33	61.1	1001	1	TP3A_HUMAN	Q13472 homo sapien
43	33	61.1	1014	1	OD01_YEAST	P20967 saccharomyc
44	33	61.1	1372	1	INSR_MOUSE	P15208 mus musculu
45	33	61.1	1382	1	INSR_HUMAN	P06213 homo sapien

ALIGNMENTS

RESULT 1
TE21_HUMAN STANDARD; PRT; 399 AA.
AC Q9Nyb0; Q8WY23; Q9NWR2;
DT 28-FEB-2003 (rel. 41, Created)
DT 28-FEB-2003 (rel. 41, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE Telomeric repeat binding factor 2 interacting protein 1 (TRF2-
DE interacting telomeric protein Rapi) (hrapi).
GN TRF2IP OR RAPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=20306633; PubMed=10850490;
RA Li B., Oestreich S., de Lange T.;
RT "Identification of human RAPI: Implications for telomere evolution.";
RL Cell 101:471-483(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=ileal mucosa;
RA Tangami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
RA Hiro M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T.,
RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Skin;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalardo S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Richardson D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RX STRUCTURE OF 132-190 BY NMR.
 RX MEDLINE=21431821; PubMed=11545594;
 RA Hanaka S., Nagado A., Yoshimura S., Aimoto S., Li B., de Lange T.,
 RA Nishimura Y.;
 RT "NMR structure of the hRap1 Myb motif reveals a canonical three-helix
 RT bundle lacking the positive surface charge typical of Myb DNA-binding
 RT domains."
 RL J. Mol. Biol. 312:167-175(2001).
 CC -1- FUNCTION: May play a role in telomere length regulation.
 CC -1- SUBUNIT: Homodimer. Binds to TRF2 (but not TRF1) with its
 CC C-terminus.
 CC -1- SUBCELLULAR LOCATION: Nuclear. Colocalizes with telomeric DNA in
 CC Interphase and metaphase cells.
 CC -1- TISSUE SPECIFICITY: Ubiquitous; highly expressed.
 CC -1- MISCELLANEOUS: Recruited to telomeres by TRF2; seemingly it does
 CC not directly bind to DNA itself.
 CC -1- SIMILARITY: Contains 1 BRC1 domain.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
 CC frameshift in position 151.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
 CC stop codon in position 299.
 CC -----
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 CC -----
 DR EMBL; AF262988; AAF72711.1; -
 DR EMBL; AF289599; AAL5783.1; ALT_FRAME.
 DR EMBL; AK000669; BAA91317.1; ALT_TERM.
 DR EMBL; BC004465; AAH04465.1; -
 DR EMBL; BC005841; AAH05841.1; -
 DR EMBL; BC022428; AAH22428.1; -
 DR PDB; 1FEK; 19-SEP-01.
 DR Genew; HGNC:19246; TERF2IP.
 DR MIM; 605061; -
 DR GO; GO:0000228; C:nuclear chromosome; TAS.
 DR GO; GO:0007004; P:telomerase-dependent telomere maintenance; TAS.
 DR GO; GO:0007003; P:telomere binding; TAS.
 DR InterPro; IPR001357; BRC1.
 DR InterPro; IPR001005; Myb DNA binding.
 DR PROSITE; PS50172; BRC1; FALSE NEG.
 DR PROSITE; PS50090; MYB_3; FALSE NEG.
 DR Nuclear protein; Chromosomal protein; Telomere; 3D-structure.
 FT DOMAIN 78 101 BRC1.
 FT DNA_BIND 128 188 MYB.
 FT DOMAIN 214 304 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 383 399 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT CONFLICT 83 83 Y -> H (IN REF. 3).
 SQ SEQUENCE 399 AA; 44260 MM; EAA615777F9D3DD CRC64;

Query Match 72.2%; Score 39; DB 1; Length 399;
 Best Local Similarity 62.5%; Pred. No. 7;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCNEDPPT 9
 DB 279 MCDDDPPT 286

RESULT 2
 IL2A_HUMAN STANDARD; PRT; 272 AA.
 IL2A_HUMAN
 AC P01589;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha
 DE subunit) (P55) (TAC antigen) (CD25 antigen).
 GN IL2RA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=85012734; PubMed=6090949;
 RA Nkaido T., Shimizu A., Ishida N., Sabe H., Teshigawara K., Maeda M.,
 RA Uchiyama T., Yodoi J., Honjo T.;
 RT "Molecular cloning of cDNA encoding human interleukin-2 receptor."
 RT Nature 311:631-635(1984).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=85012733; PubMed=6090948;
 RA Leonard W.J., Depper J.M., Crabtree G.R., Rudikoff S., Pumphrey J.,
 RA Robb R.J., Krenke M., Svetlik P.B., Peffer N.J., Waldmann T.A.,
 RA Greene W.C.;
 RT "Molecular cloning and expression of cDNAs for the human
 RT interleukin-2 receptor."
 RT Nature 311:626-631(1984).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86067183; PubMed=2999698;
 RA Ishida N., Kanamori H., Noma T., Nkaido T., Sabe H., Suzuki N.,
 RA Shimizu A., Honjo T.;
 RT "Molecular cloning and structure of the human interleukin 2 receptor
 RT gene."
 RT Nucleic Acids Res. 13:7579-7589(1985).
 RN [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86018688; PubMed=2996141;
 RA Leonard W.J., Depper J.M., Kanehisa M., Krenke M., Peffer N.J.,
 RA Svetlik P.B., Sullivan W.M., Greene W.C.;
 RT "Structure of the human interleukin-2 receptor gene."
 RT Science 230:633-639(1985).
 RN [5]
 RN SEQUENCE OF 1-21 FROM N.A.
 RX MEDLINE=87159546; PubMed=3030566;
 RA Cross S.L., Feinberg M.B., Wolf J.B., Holbrook N.J., Wong-Stall F.,
 RA Leonard W.J.;
 RT "Regulation of the human interleukin-2 receptor alpha chain promoter:
 RT activation of a nonfunctional promoter by the transactivator gene of
 RT HTLV-I.".
 RT Cell 49:47-56(1987).
 RN [6]
 RN 3D-STRUCTURE MODELING OF 23-83.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamdrough P., Hedgcock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling."
 RT Structure 2:839-851(1994).
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
 CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
 CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
 CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
 CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
 CC WITH A GAMMA CHAIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD25 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd25.htm".
 CC -----
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CC -----
DR EMBL; X01057; CA25525.1; -
DR EMBL; X01131; CA26906.1; -
DR EMBL; X01132; CA26906.1; JOINED.
DR EMBL; X01133; CA26906.1; JOINED.
DR EMBL; X01134; CA26906.1; JOINED.
DR EMBL; X01135; CA26906.1; JOINED.
DR EMBL; X01136; CA26906.1; JOINED.
DR EMBL; X01137; CA26906.1; JOINED.
DR EMBL; X01138; CA26906.1; JOINED.
DR EMBL; X01122; AAB5935.1; ALT_SEQ.
DR EMBL; X01066; AAA67527.1; -
DR EMBL; M10322; AAA67527.1; JOINED.
DR EMBL; M1060; AAA67527.1; JOINED.
DR EMBL; M1061; AAA67527.1; JOINED.
DR EMBL; M1062; AAA67527.1; JOINED.
DR EMBL; M1063; AAA67527.1; JOINED.
DR EMBL; M1064; AAA67527.1; JOINED.
DR EMBL; M1065; AAA67527.1; JOINED.
DR EMBL; M15864; AAA59162.1; -
DR PIR; A44186; UNH02.
DR PDB; 11LM; 26-JAN-95.
DR PDB; 11LN; 26-JAN-95.
DR Genew; HGNC; 6008; IL2RA.
DR MIM; 147730; -
DR MIM; 606367; -
DR GO; GO:0005886; Ciplasma membrane; TAS.
DR GO; GO:0004911; F:interleukin-2 receptor activity; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 2.
DR SMART; SM00032; CCP; 2.
DR Tramebrane; Glycoprotein; Receptor; Repeat; Signal; Sushi;
KW 3D-structure.
FT CHAIN 1 21 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 272 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 241 259 POTENTIAL.
FT DOMAIN 260 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 124 185 SUSHI 1.
FT DISULFID 224 67 SUSHI 2.
FT DISULFID 151 80 BY SIMILARITY.
FT DISULFID 125 168 BY SIMILARITY.
FT DISULFID 152 184 BY SIMILARITY.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT STRAND 35 36
FT TURN 43 44
FT STRAND 46 50
FT STRAND 64 67
FT STRAND 70 70
FT TURN 71 72
FT STRAND 73 73
FT STRAND 76 76
SQ SEQUENCE 272 AA; 30819 MW; 83D907C8C81D2C0E CRC64;

Query Match 70.4%; Score 38; DB 1; Length 272;
Best Local Similarity 62.5%; Pred. No. 7;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 QUCNEDPP 8
Db 22 ELCDDDPP 29

```

RESULT 3
YABS_SCHPO

```

ID YABS_SCHPO STANDARD; PRT; 701 AA.
AC 009807;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C2G11.05c in chromosome I.
GN SPAC2G11.05c.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leacher S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Wolkaert G., Aert R., Robben J., Grynoprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambut R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motter S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore C., Hurst S.M.,
RA Lucas M., Rochet M., Gailardin C., Tallada V.A., Garcon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).

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DR EMBL; Z54354; CA91170.1; -
DR PIR; T38571; S62460.
DR GeneDB; SPombe; SPAC2G11.05c; -
DR InterPro; IPR004328; BRO1.
DR Pfam; PF03097; BRO1. 1.
KW Hypothetical protein.
SQ SEQUENCE 701 AA; 81769 MW; E13B4CAE085671 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 701;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 LCNEDPP 8
Db 122 LCNEDPP 128

```

RESULT 4
ID ODO1_HUMAN STANDARD; PRT; 1002 AA.
ID ODO1_HUMAN
AC 002218;
DT 01-JUL-1993 (Rel. 26, Created)

ID IL2A_FELCA STANDARD; PRT; 275 AA.
 AC P41690;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
 GN IL2RA.
 OS *Felis silvestris catus* (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NC NCB1_Taxid=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matsumoto Y., Ohno K., Gotsuka R., Hirota Y., Teujimoto H., Hasegawa A.;
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
 CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE WITH A GAMMA CHAIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.
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 CC -----
 DR EMBL; D16143; BA03714.1; -
 DR HSSP; P01589; IILM.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00084; sushi; 2.
 DR SMART; SM00032; CCP; 2.
 DR KMW Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
 FT SIGNAL 1 21
 FT CHAIN 22 275
 FT DOMAIN 22 243 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
 FT TRANSMEM 244 262 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 263 275 POTENTIAL.
 FT DOMAIN 23 78 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 122 185 SUSHI 1.
 FT DISULFID 24 67 SUSHI 2.
 FT DISULFID 751 80 BY SIMILARITY.
 FT DISULFID 125 168 BY SIMILARITY.
 FT DISULFID 152 184 BY SIMILARITY.
 FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 70 70 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 275 AA; 30817 MW; C978BD8D06332326 CRC64;
 Query Match 66.7%; Score 36; DB 1; Length 275;
 Best Local Similarity 62.5%; Pred. No. 17;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QLCNEDPT 8
 DB 22 ELCDENPP 29
 RESULT 7
 TPST CAEBL STANDARD; PRT; 359 AA.
 AC Q20351;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Putative protein-tyrosine sulfotransferase (EC 2.8.2.20)
 DE (Tyrosylprotein sulfotransferase) (TPST).

GN F4269.8.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea; Rhabditidae; Peloderae; Caenorhabditis.
 NC NCB1_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Bristol N2.
 RA Taich A.;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE O-SULFATION OF TYROSINE RESIDUES WITHIN ACIDIC MOTIFS OF POLYPEPTIDES (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyrosine = adenosine 3',5'-bisphosphate + protein tyrosine-O-sulfate.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY.
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 CC -----
 DR EMBL; U00051; AAA91354.1; -
 DR PIR; T16350; T16350.
 DR WormPeP; F4269.8; CE07235.
 DR InterPro; IPR000863; Sulfotransferase.
 DR Pfam; PF00685; Sulfotransfer; 1.
 DR KMW Hypothetical protein; Transferase; Transmembrane; Glycoprotein;
 FT SIGNAL-ANCHOR 1 27
 FT DOMAIN 28 48
 FT TRANSMEM 28 48
 FT TRANSMEM 49 359
 FT DOMAIN 49 359
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 SQ SEQUENCE 359 AA; 41469 MW; 9FC2F44539B8CC53 CRC64;
 Query Match 66.7%; Score 36; DB 1; Length 359;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLCNEDPT 9
 DB 166 RLCNKDPT 174
 RESULT 8
 TPST DROME STANDARD; PRT; 385 AA.
 AC Q9YVE7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable protein-tyrosine sulfotransferase (EC 2.8.2.20)
 DE (Tyrosylprotein sulfotransferase) (TPST).
 GN CG32632/CG1573.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Gelinker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA April J.F., Agbayan A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Buam D.A., Butler H., Cadieu E., Cente A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fiedler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gloder A., Gong F., Gottell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jallat M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Moruklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gbabe R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RT Science 287:2185-2195(2000).
 CC -1- FUNCTION: CATALYZES THE O-SULFATION OF TYROSINE RESIDUES WITHIN
 CC ACIDIC MOTIFS OF POLYPEPTIDES (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyrosine =
 CC adenosine 3',5'-bisphosphate + protein tyrosine-O-sulfate.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY.
 CC
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 CC
 CC EMBL: AE003493; AAF48286.1; -
 CC FlyBase: FBgn0052632; CG32632.
 CC InterPro: IPR000863; Sulfotransferase.
 CC Pfam: PF00685; Sulfotransferase.1.
 CC DR Hypothetical protein; transferase; Transmembrane; Glycoprotein;
 CC K0 Signal-anchor.
 CC KW
 CC FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT DOMAIN 31 385 (POTENTIAL).
 CC FT FT LUMENAL, CATALYTIC (POTENTIAL).
 CC FT POLY-ALA.
 CC SQ SEQUENCE 385 AA; 44054 MW; 35BAE2B3E2D2FE1C CRC64;
 CC
 CC Query Match 66.7%; Score 36; DB 1; Length 385;
 CC Best Local Similarity 66.7%; Pred. No. 24;
 CC Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

AC 077081; Q9NEW9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-tyrosine sulfotransferase A (EC 2.8.2.20) (Tyrosylprotein
 DE sulfotransferase-A) (TPST-A).
 OS Y11B2A.15.
 GN *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Ploaderinae; *Caenorhabditis*.
 OC NCBI_TaxID=6239;
 OK
 RN
 RP SEQUENCE FROM N.A.
 RC SPRAIN-Bristol N2;
 RX MEDLINE=98406128; PubMed=9733778;
 RA Ouyang Y.-B., Moore K.L.;
 RT "Molecular cloning and expression of human and mouse tyrosylprotein
 RT sulfotransferase-2 and a tyrosylprotein sulfotransferase homologue in
 RT *Caenorhabditis elegans*."
 RT J. Biol. Chem. 273:24770-24774(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Sulston J.E.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3].
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE O-SULFATION OF TYROSINE RESIDUES WITHIN
 CC ACIDIC MOTIFS OF POLYPEPTIDES.
 CC -1- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyrosine =
 CC adenosine 3',5'-bisphosphate + protein tyrosine-O-sulfate.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY.
 CC
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 CC
 CC EMBL: AF049709; AAC36062.1; -
 CC DR EMBL: AL132804; CAC35844.1; -
 CC DR PIR: T42755; T42755.
 CC DR WormPep: Y11B2A.15; CE26632.
 CC DR InterPro: IPR000863; Sulfotransferase.
 CC Pfam: PF00685; Sulfotransferase.1.
 CC KW transferase; Transmembrane; Glycoprotein; Signal-anchor.
 CC FT DOMAIN 1 6
 CC FT TRANSMEM 7 27 CYTOPLASMIC (POTENTIAL).
 CC FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT DOMAIN 28 380 (POTENTIAL).
 CC FT CARBOHYD 66 66 LUMENAL, CATALYTIC (POTENTIAL).
 CC FT N-LINKED (GLCNAC...) (POTENTIAL).
 CC SQ SEQUENCE 380 AA; 43313 MW; FF709BF00F1EDC95 CRC64;
 CC
 CC Query Match 64.8%; Score 35; DB 1; Length 380;
 CC Best Local Similarity 66.7%; Pred. No. 36;
 CC Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
 ID TSPA_CAEEL STANDARD; PRT; 380 AA.
 ID TSPA_CAEEL STANDARD; PRT; 380 AA.

RESULT 10
 ID TE21_MOUSE STANDARD; PRT; 393 AA.
 ID TE21_MOUSE STANDARD; PRT; 393 AA.
 AC Q91VB8; Q9JTE8; Q9JTE9;
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Telomeric repeat binding factor 2 interacting protein 1 (TRF2-
 *DB Interacting telomeric protein RAPI).
 GN TRF2IP OR RAPI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L.H., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavani T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE OF 1-280 FROM N.A.
 RC STRAIN=C57BL/6;
 RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
 RA Hashimoto K.;
 RT "Isolation of full-length cDNA clones from mouse brain cDNA library
 made by oligo-capping method.";
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May play a role in telomere length regulation.
 CC -1- SUBUNIT: Homodimer. Binds to TRF2 (but not TRF1) with its
 CC C-terminus (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear. Colocalizes with telomeric DNA in
 CC interphase and metaphase cells (By similarity).
 CC -1- MISCELLANEOUS: Recruited to telomeres by TRF2; seemingly it does
 CC not directly bind to DNA itself (By similarity).
 CC -1- SIMILARITY: Contains 1 BRCT domain.
 CC -1- SIMILARITY: Contains 1 Myb-like domain.
 CC -----
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 CC -----
 CC EMBL, BC012270; AAH12270.1; -;
 DR EMBL, BC017641; AAH17641.1; -;
 DR EMBL, AB041557; BAA95042.1; -;
 DR EMBL, AB041559; BAA95043.1; ALT_INT.
 DR MGD: MGI:1929871; Tef2ip.
 DR InterPro: IPR001357; BRCT.
 DR InterPro: IPR001005; Myb_DNA_binding.
 DR PROSITE: PSS0172; BRCT; FALSE NEG.
 DR PROSITE: PSS0090; MYB_3; FALSE NEG.
 KW Nuclear protein; Chromosomal protein; Telomere.
 FT DOMAIN 78 101 BRCT.
 FT DNA_BIND 125 185 MYB.
 FT DOMAIN 232 297 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 377 393 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT CONFLICT 281 286 PTPBED -> HTHTOS (IN REF. 2).
 SQ SEQUENCE 393 AA; 43353 MW; 7A15CFD83733BE2D CRC64;
 Query Match 64.8%; Score 35; DB 1; Length 393;
 Best Local Similarity 62.5%; Pred. No. 38;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LCNEDPPT 9
 Db 275 MCDGDPPT 282
 RESULT 11
 KC33 RABIT STANDARD; PRT; 491 AA.
 ID KC33 RABIT
 AC 09T17;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Potassium voltage-gated channel subfamily S member 3 (Potassium
 DE channel Kv9.3) (Delayed-rectifier K+ channel alpha subunit 3).
 GN KCNS3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Corneal epithelium;
 RA Rae U.L.;
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Potassium channel subunit. Modulates channel activity
 CC and reduces the ion flow (By similarity).
 CC -1- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form
 CC homomultimers. Might also bind to other channel proteins (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the
 CC plasma membrane but remain in an intracellular compartment in the
 CC absence of KCNB1 (By similarity).
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL, AF209723; AAF22833.1; -;
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR001822; K+channel_pore.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003111; K_tetra.
 DR InterPro: IPR003971; Kv9_channel.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR005820; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01494; KV9CHANNEL.
 DR PRINTS: PR01491; KVCHANNEL.
 DR SMART: SM00225; BTB; 1.
 DR Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;
 FT DOMAIN 1 185 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 186 206 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 224 244 SEGMENT S2 (POTENTIAL).

FT DOMAIN 245 253 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 254 274 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 288 308 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 309 323 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 324 344 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 358 378 SEGMENT H5 (POT-FORMING) (POTENTIAL).
 FT TRANSMEM 386 406 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 407 491 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 491 AA; 55941 MW; 2EB396E089D6F77 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 491;
 Best Local Similarity 83.3%; Pred. No. 48;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPP 8
 Db 424 CSEDEPP 429

RESULT 12
 3 RAT
 NC KCS3 RAT STANDARD; PRT; 491 AA.
 NC 088759; 054900; (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Potassium voltage-gated channel subfamily S member 3 (Potassium channel Kv3.3) (Delayed-rectifier K+ channel alpha subunit 3).
 GN KCN3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=98031889; PubMed=9362476;
 RA Patel A.J., Lazdunski M., Honore E.;
 RT "Kv2.1/Kv9.3, a novel ATP-dependent delayed-rectifier K+ channel in oxygen-sensitive pulmonary artery myocytes";
 RL EMBL J. 16:6615-6625(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98369652; PubMed=9704029;
 RA Stocker M., Kerscheneitner D.;
 RT "Cloning and tissue distribution of two new potassium channel alpha-subunits cloned from rat brain";
 DE Biochem. Biophys. Res. Commun. 248:927-934(1998).
 DE FUNCTION: Potassium channel subunit. Modulates channel activity and shifts the activation threshold of KCNB1 to more negative values.
 GN SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form homomultimers. Might also bind to other channel proteins (By similarity).
 OC SUBCELLULAR LOCATION: Integral membrane protein. May not reach the plasma membrane but remain in an intracellular compartment in the absence of KCNB1 (By similarity).
 CC TISSUE SPECIFICITY: Detected in lung, spleen, brain and heart.
 CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.
 CC -1- MISCELLANEOUS: Inhibited by 4-aminopyridine (4-AP). Channel activity is reversibly inhibited by hypoxia and down-regulated in the absence of intracellular ATP.
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.

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CC or send an email to license@isb-sib.ch.
 CC EMBL AF029056; AAB94882.1; -
 DR EMBL Y17607; CA176805.1; -
 DR InterPro: IPR000210; BTB_PQZ.
 DR InterPro: IPR005821; Ion trans.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K channel.
 DR InterPro: IPR003131; K tetra.
 DR InterPro: IPR003971; Kv3 channel.
 DR InterPro: IPR003968; Kv channel.
 DR InterPro: IPR005820; M+channel_nlg.
 DR Pfam: PF00520; Ion trans. 1.
 DR Pfam: PF02214; K tetra. 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01494; KVCHANNEL.
 DR PRINTS: PR01491; KVCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;
 KM Multigene family.
 FT DOMAIN 1 185 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 186 206 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 224 244 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 245 253 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 254 274 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 288 308 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 309 323 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 324 344 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 358 378 SEGMENT H5 (POT-FORMING) (POTENTIAL).
 FT TRANSMEM 385 405 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 406 491 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 113 113 I -> F (IN REF. 1).
 SQ SEQUENCE 491 AA; 55865 MW; 6157BC7EF94CC2B CRC64;

Query Match 64.8%; Score 35; DB 1; Length 491;
 Best Local Similarity 83.3%; Pred. No. 48;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CNEDEPP 8
 Db 424 CSEDEPP 429

RESULT 13
 GATE_THEVO
 ID GATE_THEVO STANDARD; PRT; 598 AA.
 AC Q979L9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glucamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.-) (Glu-ADT subunit E).
 GN GATE OR TV1141 OR TVG116951.
 GN Thermoplasma volcanum.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 NX NCBI_TaxID=50339;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
 RX MEDLINE=20570466; PubMed=11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,
 RA Nunoshita T., Yamamoto Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
 RT "Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanum";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 RL FUNCTION: Allows the formation of correctly charged Gln-tRNA(Gln) through the transamidation of misacylated Glu-tRNA(Gln) in organisms which lack glutamyl-tRNA synthetase. The reaction takes place in the presence of glutamine and ATP through an activated gamma-phospho-Glu-tRNA(Gln). The gate system is

```

CC specific for glutamate and does not act on aspartate (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
CC + phosphate + L-glutaminyl-tRNA(Gln) + L-glutamate.
CC -1- SUBUNIT: Heterodimer of gatB and gatC (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GATB/GATE FAMILY. GATE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF000995; BAB60283.1; -.
CC DR HAMAP; MF_00588; -. 1.
CC DR InterPro; IPR004413; GATB.
CC DR InterPro; IPR006107; GATB-cent.
CC DR InterPro; IPR006075; GATB_N.
CC DR Pfam; PF01162; GATB; 1.
CC DR Pfam; PF02934; GATB_N; 1.
CC DR PROSITE; PS01234; GATB; 1.
CC KW Protein biosynthesis; Ligase; Complete proteome.
CC SQ SEQUENCE 598 AA; 67355 MW; 6777BB8F039F9CCF CAC64;

Query Match 64.8%; Score 35; DB 1; Length 598;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CNEDEP 8
Db 78 CDEDEP 83

RESULT 14
DPB2_YEAST
AC P24482; Q06622; STANDARD; PRT; 692 AA.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase epsilon subunit B (EC 2.7.7.7) (DNA polymerase II
DE subunit B).
GN DPB2 OR YPR175W OR P9705.7.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=YH8;
RX MEDLINE=91271241; PubMed=2052544;
RA Araki H., Hamatake R.K., Johnston L.H., Sugino A.;
RT "DPB2, the gene encoding DNA polymerase II subunit B, is required for
RT chromosome replication in Saccharomyces cerevisiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4601-4605(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SZ88C / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Busey J.R., Storms R.K., Ahmed A., Albermann K., Allen E., Ansgore W.,
RA Araujo R., Aparicio A., Bartell B.G., Badcock K., Benes V.,
RA Boeselein D., Bowman S., Brucher M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Fillesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA Hunnicke-Smith S., Hyman R., Johnston M., Kaitam S., Kleine K.,
RA Komp C., Kurd O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Nemath A., Nettwich U., Oetner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Schafte M.,

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RA Schreierens, J., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA Ureteratarau L.A., Ushinsky S., Vierendeels F., Vissers S., Vose H.,
RA Walsh S.V., Wambut R., Wang Y., Wedler E., Wedler H., Minnett E.,
RA Zhong W.W., Zollner A., Vo D.H., Hant J.,
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.,"
RA Nature 387:103-105(1997) .
CC -I- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
CC REPLICATION. DBP2 IS ESSENTIAL FOR CELL GROWTH. MAY HAVE A ROLE IN
CC DNA SYNTHESIS.
CC -I- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -I- SUBUNIT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30
CC kDa, and 29 kDa).
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
CC ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
CC DIFFERENT REACTIONS OF DNA SYNTHESIS.
CC -I- SIMILARITY: TO OTHER SPECIES DNA POLYMERASE EPSILON, SUBUNIT B.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M61710; AAA34576.1; ALT_INIT.
DR EMBL; U25842; AAB68109.1; -.
DR PIR; S59833; S59833.
DR SGD; S0006379; DPB2.
DR Pfam; PF04042; DNA_pol_E_B; 1.
DR TransEbase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Nuclear protein.
FT CONFLICT 461 461 F -> Y (IN REF. 1) .
FT FT CONFLICT 524 524 K -> R (IN REF. 1) .
FT FT CONFLICT 568 568 V -> F (IN REF. 1) .
FT FT CONFLICT 587 587 E -> Q (IN REF. 1) .
FT FT CONFLICT 647 647 T -> I (IN REF. 1) .
SQ SEQUENCE 692 AA; 78703 MW; SC01647BD2B6A39A CRC64;

Query Match 64.8%; Score 35; DB 1; Length 692;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLNEDPPT 9
Db 425 QKLNDDPPT 433

RESULT 15
SRB9_YEAST STANDARD; PRT; 1420 AA.
ID SRB9_YEAST
AC P38931;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Suppressor of RNA polymerase B SRB9 (SCA1 protein).
GN SRB9 OR SCA1 OR SSN2 OR YDR443C.
OS Saccharomyces cerevisiae (Baker's yeast) .
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95293223; PubMed=7774808;
RA Hegnatter C.J., Thompson C.M., Zhang J., Chao D.M., Liao S.-M.,
RA Koloske A.J., Okamura S., Young R.A.;
RA "Association of an activator with an RNA polymerase II holoenzyme.,"
RA Genes Dev. 9:897-910(1995) .
RL [2]
RN SEQUENCE FROM N.A.
RP

```

RA Yuryev A., Gorden J.L.;
 RN Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.

[3]
 RE SEQUENCE FROM N.A.

RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,

RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,

RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,

RA Mosedale D., Nakahara K., Namach A., Oefner P., Oh C., Petel F.X.,

RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,

RA Winant A., Yelton M., Boetstein D., Davis R.W.;

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COMPONENT OF THE RNA POLYMERASE II HOLOENZYME AND THE

CC MEDITOR OF ACTIVATION SUBCOMPLEX.

CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U23812; AAA91316.1; -

DR EMBL; U09176; AAA18614.1; -

DR EMBL; U33007; AAB64875.1; -

DR PIR; B57062; B57062.

DR TRNSPAC; T02153; -

DR GSD; S0002851; SSN2.

KW Nuclear protein.

FT DOMAIN 526 529 POLY-ASN.

FT DOMAIN 657 664 POLY-GLU.

FT DOMAIN 813 816 POLY-SER.

FT DOMAIN 1005 1008 POLY-LEU.

FT DOMAIN 1121 1136 POLY-GLN.

FT CONFLICT 38 38 D -> E (IN REF. 2).

FT CONFLICT 812 812 E -> V (IN REF. 2).

FT CONFLICT 859 859 T -> S (IN REF. 2).

FT CONFLICT 877 878 VK -> GE (IN REF. 2).

FT CONFLICT 887 887 T -> P (IN REF. 2).

FT CONFLICT 1284 1284 Y -> S (IN REF. 2).

SO SEQUENCE 1420 AA; 160000 MW; 7F6CFABBE0FAC918 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 1420;

Best Local Similarity 75.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 QLCNEDDP 8

985 KLTNEDDP 992

Search completed: September 10, 2003, 17:40:53
 Job time : 10 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:38:22 ; Search time 12.15 Seconds
(without alignments)
71.236 Million cell updates/sec

Title: US-09-759-112a-36

Perfect score: 54

Sequence: 1 OLCNEDDPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	1009	2 T40412	2-oxoglutarate dehydrogenase el component - fission yeast (Schizosaccharomyces pombe)
2	39	72.2	102	4 A37413	hypothetical RTVL-H3 promoter region/calbindin fusion protein - human (fragment)
3	39	72.2	490	2 T40116	hypothetical protein - human (fragment)
4	38	70.4	272	1 UH02	interleukin-2 receptor - human (fragment)
5	37	68.5	701	2 S62460	hypothetical protein - human (fragment)
6	37	68.5	895	2 T45738	hypothetical protein - human (fragment)
7	37	68.5	1003	2 A38234	oxoglutarate dehydrogenase el component - fission yeast (Schizosaccharomyces pombe)
8	37	68.5	1022	2 T49683	probable oxoglutarate dehydrogenase el component - fission yeast (Schizosaccharomyces pombe)
9	36	66.7	245	2 T26868	hypothetical protein - human (fragment)
10	36	66.7	359	2 T16350	hypothetical protein - human (fragment)
11	35	64.8	185	2 T10677	pathogenesis-related protein - human (fragment)
12	35	64.8	283	2 C75518	stromelysin 3-kDa fragment - human (fragment)
13	35	64.8	334	2 T11633	hypothetical protein - human (fragment)
14	35	64.8	380	2 T42755	tyrosylprotein sulfotransferase - human (fragment)
15	35	64.8	491	2 U80276	voltage-gated potassium channel - human (fragment)
16	35	64.8	692	1 B57062	DNA-directed DNA polymerase - human (fragment)
17	35	64.8	1420	2 B57062	SRB9 protein - yeast (fragment)
18	35	64.8	2055	2 T00093	hypothetical protein - human (fragment)
19	34	63.0	275	1 J01113	interleukin-2 receptor - human (fragment)
20	34	63.0	322	1 S07442	interleukin-2 receptor - human (fragment)
21	34	63.0	322	2 AB0697	probable proteinase - human (fragment)
22	34	63.0	340	2 T37966	transcription factor - human (fragment)
23	34	63.0	397	2 S20617	MDR-type perase - human (fragment)
24	34	63.0	472	2 C97311	hypothetical protein - human (fragment)
25	34	63.0	701	2 T37882	hypothetical protein - human (fragment)
26	34	63.0	730	2 S48813	hypothetical protein - human (fragment)
27	34	63.0	860	2 J04566	chitinase (EC 3.2.1.15) - human (fragment)
28	34	63.0	962	2 T00262	hypothetical protein - human (fragment)
29	34	63.0	1003	2 T13951	DNA topoisomerase - human (fragment)

30	34	63.0	1928	2 J06010	beta-galactosidase
31	33	61.1	112	2 S19971	Ig kappa chain V region - human (fragment)
32	33	61.1	131	2 PH1226	Ig kappa chain pre - human (fragment)
33	33	61.1	161	2 E85354	PR-1-like protein - human (fragment)
34	33	61.1	161	2 H84518	pathogenesis-related protein - human (fragment)
35	33	61.1	161	2 T52399	pathogenesis-related protein - human (fragment)
36	33	61.1	163	2 T04989	pathogenesis-related protein - human (fragment)
37	33	61.1	168	2 A24620	pathogenesis-related protein - human (fragment)
38	33	61.1	168	2 C24620	pathogenesis-related protein - human (fragment)
39	33	61.1	168	2 B24620	pathogenesis-related protein - human (fragment)
40	33	61.1	169	2 F87713	conserved hypothetical protein - human (fragment)
41	33	61.1	173	2 S47171	gene PR-1 protein - human (fragment)
42	33	61.1	174	2 S71554	pathogenesis-related protein - human (fragment)
43	33	61.1	175	2 S43894	pathogenesis-related protein - human (fragment)
44	33	61.1	177	2 S04728	pathogenesis-related protein - human (fragment)
45	33	61.1	177	2 T08126	pathogenesis-related protein - human (fragment)

ALIGNMENTS

RESULT 1
T40412
2-oxoglutarate dehydrogenase el component - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C/Accession: T40412
R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Submitted to the EMBL Data Library, August 1998
A/Reference number: Z21926
A/Accession: T40412
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1009 <LVN>
A/Cross-references: EMBL:AL01261; PIDN:CAA20299.1; GSPDB:GN00067; SPDB:SPBC3H7.03c
A/Experimental source: strain 972h-; cosmid C3H7
C/Genetics:
A/Genes: SPDB:SPBC3H7.03c
A/Map position: 2
C/Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding domain

Query Match
Best Local Similarity 77.8%; Score 42; DB 2; Length 1009;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 792 OLCNEDP 798

RESULT 2
A37413
hypothetical RTVL-H3 promoter region/calbindin fusion protein - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
C/Accession: A37413
R/Liu, A.Y.; Abraham, B.A.
Cancer Res. 51, 4107-4110, 1991
A/Title: Subtractive cloning of a hybrid human endogenous retrovirus and calbindin gene
A/Reference number: A37413; MUID:91309099; PMID:1713126
A/Accession: A37413
A/Molecule type: mRNA
A/Residues: 1-102 <LIU>
A/Cross-references: GB:S46006; NID:G1679976; PIDN:AB19408.1; PID:G233226
A/Experimental source: prostate bone metastasis cell line PC3
A/Note: sequence extracted from NCBI backbone (NCBIN:46006, NCBI:46012)
C/Keywords: fusion protein
F:1-50/Region: retrovirus-like H3 promoter region derived
F:51-102/Region: human calbindin-derived (fragment)

Query Match
Best Local Similarity 72.2%; Score 39; DB 4; Length 102;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPT 9
DB 25 LCNEDEPT 32

RESULT 3
T40116
hypothetical protein SPBC2D10.13 - fission yeast (Schizosaccharomyces pombe)
C/Spectes: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C/Accession: T40116
R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D.
submitted to the EMBL Data Library, September 1998
A/Reference number: Z21906
A/Accession: T40116
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-490 <MOO>
A/Cross-references: EMBL:AL031788; PIDN:CAA21171.1; GSPDB:GN00067; SPDB:SPBC2D10.13
Experimental source: strain 972n-; cosmid c2D10
Genetics:
A/Map position: 2
A/Map position: 2
A/Intons: 84/3
C/Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC2D10.13

Query Match 72.2%; Score 39; DB 2; Length 490;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCNEDEPT 8
DB 237 LCSEDEPT 243

RESULT 4
UHH2
interleukin-2 receptor alpha chain precursor [validated] - human
N/Alternate names: CD25; Tac antigen
N/Containing: Interleukin-2 receptor alpha chain, splice form 2
C/Spectes: Homo sapiens (man)
C/Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C/Accession: A44186; A24113; A01856; I57801; I52791; A61346; A33651; A34861; I52255
R/Leonard, W.J.; Depper, J.M.; Kanehisa, M.; Koenke, M.; Pelfer, N.J.; Svetlik, P.B.; S
Science 220, 633-639, 1985
A/Title: Structure of the human interleukin-2 receptor gene.
A/Reference number: A44186; MUID:86018860; PMID:2996141
A/Accession: A44186
Molecule type: DNA
A/Residues: 1-272 <LEO>
A/Cross-references: GB:M10322
R/Ishida, N.; Kanamori, H.; Noma, T.; Nakaide, T.; Sabe, H.; Suzuki, N.; Shimizu, A.; Hc
Nucleic Acids Res. 13, 7579-7589, 1985
A/Title: Molecular cloning and structure of the human interleukin 2 receptor gene.
A/Reference number: A24113; MUID:86061183; PMID:2999698
A/Accession: A24113
A/Molecule type: DNA
A/Residues: 1-272 <ISH>
A/Cross-references: GB:X01331; NID:G33818; PIDN:CAA26906.1; PID:G1200070
R/Nakaide, T.; Shimizu, A.; Ishida, N.; Sabe, H.; Teshigawara, K.; Maeda, M.; Uchiyama,
Nature 311, 631-635, 1984
A/Title: Molecular cloning of cDNA encoding human interleukin-2 receptor.
A/Reference number: A01856; MUID:85012734; PMID:6090949
A/Accession: A01856
A/Molecule type: mRNA
A/Residues: 1-272 <NIK>
A/Cross-references: GB:X01057; GB:X01058; GB:X01402; NID:G33812; PIDN:CAA25525.1; PID:G3
R/Cosman, D.; Wignall, J.; Lewis, A.; Albert, A.; Cerretti, D.P.; Park, L.; Power, S.K.;
Mol. Immunol. 23, 935-941, 1986
A/Title: High level stable expression of human interleukin-2 receptors in mouse cells ge
A/Reference number: I57801; MUID:87064653; PMID:3097520
A/Accession: I57801

A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 22-125, 'K', 127-262, 'Q', 264-272 <COS>
A/Cross-references: GB:M14098; NID:G186307; PIDN:AAA59142.1; PID:G386820
R/Cross, S.L.; Feinberg, M.B.; Wolf, J.B.; Holbrook, N.U.; Wong-Staal, F.; Leonard, W.J
Cell 49, 47-56, 1987
A/Title: Regulation of the human interleukin-2 receptor alpha chain promoter: activation
A/Reference number: I52791; MUID:87159546; PMID:3030566
A/Accession: I52791
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-21 <CRO>
A/Cross-references: GB:M1864; NID:G186375; PIDN:AAA59162.1; PID:G553510
R/Urdal, D.L.; March, C.J.; Gillis, S.; Larsen, A.; Dower, S.K.
Proc Natl. Acad. Sci. U.S.A. 81, 6481-6485, 1984
A/Title: Purification and chemical characterization of the receptor for interleukin 2 fr
A/Reference number: A61346; MUID:85038539; PMID:6436815
A/Accession: A61346
A/Molecule type: protein
A/Residues: 22-31 <URD>
R/Miedel, M.C.; Hulmes, J.D.; Weber, D.V.; Bailon, P.; Pan, Y.C.E.
Biochem. Biophys. Res. Commun. 154, 372-379, 1988
A/Title: Structural analysis of recombinant soluble human interleukin-2 receptor. Primar
A/Reference number: A33651; MUID:88280794; PMID:3134887
A/Accession: A33651
A/Molecule type: protein
A/Residues: 22-244, 'P', <MIE1>
A/Note: this soluble recombinant form binds IL-2
R/Miedel, M.C.; Hulmes, J.D.; Pan, Y.C.E.
J. Biol. Chem. 264, 21097-21105, 1989
A/Title: Limited proteolysis of recombinant human soluble interleukin-2 receptor. Identit
A/Reference number: A34186; MUID:90078206; PMID:2687272
A/Accession: A34186
A/Molecule type: protein
A/Residues: 22-26; 58-62; 109-113; 119-123; 162-166 <MIE2>
A/Note: use of recombinant protein and proteolysis allowed the authors to study the reg
R/Mercken, L.; Moraes, V.; Hemon, L.; Lionne, B.; Bousseau, A.; Dautry-Varsat, A.; Collin
Biochem. Biophys. Res. Commun. 180, 1390-1395, 1991
A/Title: An exon 5-deleted mRNA encodes a functional interleukin 2 receptor alpha-subunit
A/Reference number: I52255; MUID:92062171; PMID:1840490
A/Accession: I52255
A/Status: translation not shown; translated from GB/EMBL/DBJ
A/Residues: 193-194, 219-220 <MER>
A/Molecule type: mRNA
A/Residues: 193-194, 219-220 <MER>
A/Cross-references: GB:S64248; NID:G238639; PIDN:AA80279.1; PID:G238640
C/Comment: This receptor is sulfated, phosphorylated, and contains N- and O-linked carb
C/Genetics:
A/Gene: GDB:IL2RA
A/Cross-references: GDB:119345; OMIM:147730
A/Map position: 10p15-10p14
A/Intons: 22/1; 86/1; 123/1; 195/1; 219/1; 243/1; 265/2
C/Complex: The high affinity receptor is a heterotrimer of alpha, beta (see PIR:A3042),
C/Function:
A/Description: receptor for interleukin-2
A/Pathway: Interleukin-2 stimulated growth and differentiation of T cells, B cells, NK
C/Superfamily: Interleukin-2 receptor alpha chain; complement factor H repeat homology
C/Keywords: alternative splicing; cytokine receptor; duplication; glycoprotein; heterotr
F,1-21/Domain: signal sequence #status predicted <Sig>
F,19-82/Domain: complement factor H repeat homology <FHI>
F,22-272/Product: interleukin-2 receptor alpha chain #status experimental <MAT1>
F,22-272/Domain: extracellular #status predicted <EXT>
F,22-194,219-272/Product: interleukin-2 receptor alpha chain, splice form 2 #status pred
F,22-88,119-187/Region: interleukin-2 binding core
F,125-184/Domain: complement factor H repeat homology <FHI2>
F,241-259/Domain: transmembrane #status predicted <TM>
F,260-272/Domain: intracellular #status predicted <INT>
F,24-168,67-125,152-184/Dissulfide bonds: #status experimental
F,49-80,51-82/Dissulfide bonds: (or 49-82, 51-80) #status experimental
F,70,89/Binding site: carbohydrate (Asn) (covalent) #status experimental
F,218,224,229,236,237/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 70.4%; Score 38; DB 1; Length 272;
Best Local Similarity 62.5%; Pred. No. 16;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 QLCNEDPP 8
:|||||
Db 22 ELCDDDPP 29

RESULT 5
S62460
hypothetical protein SPAC2G11.05c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: T38571; S62460
R:Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: 221745
A:Accession: T38571
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-701 <BA2>
A:Cross-references: EMBL:254354; NID:G1019398; PIDN:CAA91170.1; PID:G1019403; GSPDB:GN00
A:Experimental source: strain 972h-; cosmid c2G11
C:Genetics:
A:Gene: SPAC2G11.05c
A:Map position: 1L

Query Match 68.5%; Score 37; DB 2; Length 701;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDPP 8
:|||||
Db 122 LCNEKRP 128

RESULT 6
T45738
hypothetical protein F24M12.110 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T45738
R:Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223012
A:Accession: T45738
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-895 <VIT>
A:Cross-references: EMBL:AL132980
A:Experimental source: cultivar Columbia; BAC clone F24M12
C:Genetics:
A:Map position: 3
A:introns: 435/3; 485/3; 613/1; 671/2; 762/2; 827/2
A>Note: F24M12.110

Query Match 68.5%; Score 37; DB 2; Length 895;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CNEDPPT 9
:|||||
Db 408 CPEDPPT 414

RESULT 7
A38234
oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) precursor - human
N:Alternate names: 2-oxoglutarate:lipoamide 2-oxidoeductase; alpha-ketoglutarate dehyd
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1999
C:Accession: A38234
R:Kolke, K.; Urata, Y.; Goto, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 1963-1967, 1992

A>Title: Cloning and nucleotide sequence of the cDNA encoding human 2-oxoglutarate dehyd
A:Reference number: A38234; MUID:92179301; PMID:1542694
A:Accession: A38234
A:Molecule type: mRNA
A:Residues: 1-1003 <KO1>
A:Cross-references: GB:D10523
A:Experimental source: fetal liver
A>Note: sequence extracted from NCBI backbone (NCBI:87352)
C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom
C:Keywords: mitochondrion; oxidoreductase; thiamin pyrophosphate; tricarboxylic acid cyc
F:1-4/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:41-1003/Product: oxoglutarate dehydrogenase (lipoamide) #status predicted <MAT>
F:408-453/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 68.5%; Score 37; DB 2; Length 1003;
Best Local Similarity 71.4%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLCNEDP 7
:|||||
Db 801 QWCNDPP 807

RESULT 8
T49683
probable oxoglutarate dehydrogenase precursor [imported] - Neurospora crassa
N:Alternate names: protein B8B20.370
C:Species: Neurospora crassa
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C:Accession: T49683
R:Schulte, U.; Algn, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49683
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1022 <SCH>
A:Cross-references: EMBL:AL355933; GSPDB:GN00116; NCSP:B8B20.370
A:Experimental source: BAC clone B8B20; strain OR74A
C:Genetics:
A:Gene: NCSP:B8B20.370
A:Map position: 6
A:introns: 27/3; 843/1
C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom

Query Match 68.5%; Score 37; DB 2; Length 1022;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LCNEDP 7
:|||||
Db 794 LCNEDP 799

RESULT 9
T26868
hypothetical protein Y43F8C.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26868
R:Ainscough, R.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20279
A:Accession: T26868
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-245 <WIL>
A:Cross-references: EMBL:AL032637; PIDN:CAA21609.1; CESP:Y43F8C.5
A:Experimental source: clone Y43F8C
C:Genetics:
A:Gene: CESP:Y43F8C.5
A:introns: 69/3; 163/2

Query Match 66.7%; Score 36; DB 2; Length 245;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPT 9
Db 192 LCLSDPPT 199

RESULT 10

T16350
hypothetical protein F42G9.8 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000

C/Accession: T16350

R/Taich, A.

Submitted to the EMBL Data Library, March 1996

A/Description: The sequence of *C. elegans* cosmid F42G9.

A/Reference number: Z18498

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-359 <TA1>

A/Cross-references: EMBL:U00051; NID:g1216305; PID:g1216308; PIDN:AAA91354.1; CESP:F42G9

A/Experimental source: strain Bristol N2

C/Genetics:

A/Gene: CESP:F42G9.8

A/Insertions: 28/2; 50/2; 113/2; 155/3; 220/3; 290/2

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F42G9.8

Query Match 66.7%; Score 36; DB 2; Length 359;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLCNEDEPT 9
Db 166 RLCKNDPPT 174

RESULT 11

T10677

pathogenesis-related protein homolog F3L17.40 - *Arabidopsis thaliana*

C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999

C/Accession: T10677

R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.

Submitted to the Protein Sequence Database, June 1999

A/Reference number: Z16652

A/Accession: T10677

A/Molecule type: DNA

A/Residues: 1-185 <BEV>

A/Cross-references: EMBL:AL080283; GSPDB:GN00062; ATSP:F3L17.40

A/Experimental source: cultivar Columbia; BAC clone F3L17

C/Genetics:

A/Gene: ATSP:F3L17.40

A/Map position: 4

C/Superfamily: pathogenesis-related leaf protein

Query Match 64.8%; Score 35; DB 2; Length 185;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCNEDEPT 8
Db 170 ICNIDPP 176

RESULT 12

C75518

streptomycin 3-kinase - *Deinococcus radiodurans* (strain R1)

C/Species: *Deinococcus radiodurans*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C/Accession: C75518

R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterlinden, T.; Zaleski, C.; M.

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: C75518

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-283 <WHI>

A/Cross-references: GB:AE001904; GB:AE000513; NID:g6458129; PIDN:AAF10031.1; PID:g645813

A/Experimental source: strain R1

C/Genetics:

A/Gene: DR0455

A/Map position: 1

C/Superfamily: streptomycin 6-kinase

Query Match 64.8%; Score 35; DB 2; Length 283;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCNEDEPT 9
Db 213 LCNPDPT 220

RESULT 13

T11633

hypothetical protein - fission yeast (*Schizosaccharomyces pombe*)

C/Species: *Schizosaccharomyces pombe*

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000

C/Accession: T11633

R/Barré, B.G.; Rajandream, M.A.; Wood, V.

Submitted to the EMBL Data Library, September 1997

A/Reference number: Z17303

A/Accession: T11633

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-334 <BAR>

A/Cross-references: EMBL:Z99260

C/Genetics:

A/Map position: 1L

A/Note: SPAC3A11.11c

C/Superfamily: fission yeast pyridoxine 4-dehydrogenase

Query Match 64.8%; Score 35; DB 2; Length 334;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CNEDEPT 9
Db 229 CNEQPS 235

RESULT 14

T42755

tyrosyl-protein sulfoxidase homolog - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C/Accession: T42755

R/Moore, K.L.; Ouyang, Y.B.

J. Biol. Chem. 273, 24770-24774, 1998

A/Title: Molecular cloning and expression of human and mouse tyrosyl-protein sulfoxidase

A/Reference number: Z22262; MUID:98406128; PMID:9733778

A/Accession: T42755

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-380 <MOO>

A/Cross-references: EMBL:AF049709; NID:g3617847; PIDN:AA036062.1; PID:g3617848

Query Match 64.8%; Score 35; DB 2; Length 380;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLCNEDDPT 9
 DB 155 RLCNKDPFT 163

RESULT 15

JB0276
 Voltage-gated potassium channel alpha chain Kv9.3 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 08-Dec-2000
 C:Accession: JB0276
 R:Stocker, M.; Kerchenshteiner, D.
 Biochem. Biophys. Res. Commun. 248, 927-934, 1998
 A:Title: Cloning and tissue distribution of two new potassium channel alpha-subunits fro
 A:Reference number: JB0275; PMID:9836952; PMID:9704029
 A:Accession: JB0276
 A:Molecule type: mRNA
 A:Residues: 1-491 <STO>
 Cross-references: GB:Y17607
 perfamily: potassium channel protein drk1

Query Match 64.8%; Score 35; DB 2; Length 491;
 Best Local Similarity 83.3%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CNEDDPT 8
 DB 424 CSEDDPT 429

Search completed: September 10, 2003, 17:42:44
 Job time : 14.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:37:57 : Search time 30.8 Seconds
(without alignments)
92.162 Million cell updates/sec

Title: US-09-759-112A-19
Perfect score: 55
Sequence: 1 RVSLEYAMDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	70.9	167	5 002369	002369 chironomus
2	38	69.1	164	16 082N46	082N46 salmonella
3	38	69.1	164	16 082N47	082N47 salmonella
4	37	67.3	183	4 09H616	09H616 homo sapien
5	37	67.3	190	4 09NT91	09NT91 homo sapien
6	37	67.3	322	17 097CJ6	097CJ6 thermoplasma
7	37	67.3	387	16 08DVU3	08DVU3 streptococ
8	37	67.3	391	4 09NXV7	09NXV7 homo sapien
9	37	67.3	1712	4 081Y21	081Y21 homo sapien
10	36	65.5	255	16 08DCL2	08DCL2 sulfolobus
11	36	65.5	275	17 097ZD4	097ZD4 vulvulin
12	36	65.5	286	12 09Q8H7	09Q8H7 myxoma viru
13	36	65.5	359	16 08FKD3	08FKD3 xanthomonas
14	36	65.5	454	16 09SWT9	09SWT9 streptomyces
15	35	63.6	145	5 09GUY2	09GUY2 polyanthroc
16	35	63.6	210	16 08DRS5	08DRS5 streptococ

17	35	63.6	345	16 09X7P7	09X7P7 streptomyc
18	35	63.6	332	12 091BD6	091BD6 spodoptera
19	35	63.6	432	2 09RN63	09RN63 streptomyc
20	35	63.6	556	5 081PL3	081PL3 drosophila
21	35	63.6	1216	10 08W1P1	08W1P1 oryza sativ
22	34	61.8	192	2 050403	050403 methylobact
23	34	61.8	314	16 092TR9	092TR9 rhizobium m
24	34	61.8	391	11 091V12	091V12 mus musculu
25	34	61.8	742	2 08KZS8	08KZS8 acetobacter
26	34	61.8	742	2 053362	053362 acetobacter
27	34	61.8	767	17 09H1D7	09H1D7 thermoplasma
28	34	61.8	812	16 08REC9	08REC9 fusobacteri
29	34	61.8	880	10 09FID9	09FID9 arabidopsis
30	34	61.8	880	10 08RW00	08RW00 arabidopsis
31	34	61.8	887	2 09RGU0	09RGU0 salmonella
32	34	61.8	893	2 09LSU7	09LSU7 salmonella
33	34	61.8	893	16 0935F3	0935F3 salmonella
34	34	61.8	1653	16 08XAY3	08XAY3 escherichia
35	34	61.8	1653	16 08CVT2	08CVT2 escherichia
36	33	60.0	99	2 09F8J2	09F8J2 carboxydoch
37	33	60.0	134	4 09EGJ9	09EGJ9 homo sapien
38	33	60.0	148	10 09LER7	09LER7 arabidopsis
39	33	60.0	148	10 09AB31	09AB31 arabidopsis
40	33	60.0	153	17 08TK61	08TK61 methanosa
41	33	60.0	167	5 015588	015588 entamoeba h
42	33	60.0	174	16 098GL3	098GL3 rhizobium l
43	33	60.0	178	2 09APR9	09APR9 carboxydoch
44	33	60.0	249	16 08U864	08U864 agrobacteri
45	33	60.0	293	16 086594	086594 streptomyc

ALIGNMENTS

RESULT 1

ID 002369 PRELIMINARY; PRT; 167 AA.

AC 002369; 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Globin XII.

GN CTT-12.

OS Chironomus thummi thummi (Midge).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;

OC Chironomidae; Chironominae; Chironomus.

OX NCBI_TaxID=7155;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94275867; PubMed=8006991;

RA Kao W.Y., Trewitt P.M., Bergtrom G.;

RT "Intron-containing globin genes in the insect Chironomus thummi.";

RL J. Mol. Evol. 38:241-249(1994).

RN [2]

RP SEQUENCE FROM N.A.

RA Gruhl M.C., Kao W.-Y., Bergtrom G.;

RT "Evolution of Orthologous Intronless and Intron-Bearing Globin Genes

in Two Insect Species.";

RT J. Mol. Evol. 0:0-0(1997).

DR EMBL; AF001292; AAB58934.1; -.

DR HSSP; P02229; IECA.

DR InterPro; IPR002336; Erythrcurin.

DR InterPro; IPR000971; Globin.

DR Pfam; PF00042; globin; 1.

DR PRINTS; PR00611; ERYTHCRURIN.

DR PROSITE; PS01033; GLOBIN; 1.

KW Hem; Oxygen transport; Transport

SO SEQUENCE 167 AA; 18428 MW; 551F5ASDFC3E7742 CRC64;

Query Match 70.9%; Score 39; DB 5; Length 167;
Best Local Similarity 72.7%; Pred. No. 5.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAYAMDY 11
 DB 126 RVSLTAYLADH 136

RESULT 2

Q8ZN46 PRELIMINARY; PRT; 1644 AA.
 AC Q8ZN46;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Putative inner membrane lipoprotein.
 GN STM2532.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 [1]

SEQUENCE FROM N.A.
 STRAIN=L72 / SCS1412 / ATCC 700720;
 MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewel N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2."
 RL Nature 413:852-856(2001).
 DR EMBL; AB008815; AAL21426.1; -
 KM Lipoprotein; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1644 AA; 179646 MW; BCF7A526BD629CA1 CRC64;

Query Match 69.1%; Score 38; DB 16; Length 1644;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTVAYAMDY 11
 DB 1245 LTVAYAMDY 1252

RESULT 3
 Q8Z4N7 PRELIMINARY; PRT; 1644 AA.
 Q8Z4N7;
 01-MAR-2002 (TReMBLrel. 20, Created)
 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Putative lipoprotein.
 GN STY2778.
 OS Salmonella typh.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 [1]

SEQUENCE FROM N.A.
 STRAIN=CT18;
 MEDLINE=21534947; PubMed=11677608;
 RA Churchil J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churchil J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Baker S., Baeham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.W., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
 RA Krogh A., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18."
 RL Nature 413:848-852(2001).
 DR EMBL; AL627275; CAD02735.1; -

KW Lipoprotein; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1644 AA; 179378 MW; D8341677631A70DF CRC64;

Query Match 69.1%; Score 38; DB 16; Length 1644;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTVAYAMDY 11
 DB 1245 LTVAYAMDY 1252

RESULT 4

Q9H616 PRELIMINARY; PRT; 183 AA.
 AC Q9H616;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ22680.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]

SEQUENCE FROM N.A.
 RC TISSUE=Small Intestine;
 RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
 RA Suzuki Y., Ohtsushi M., Nishi T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Isegaai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK026333; BAB15451.1; -
 DR EMBL; BC020601; AAB20601.1; -
 KM Hypothetical protein.
 SQ SEQUENCE 183 AA; 20827 MW; 6E33085B02A41194 CRC64;

Query Match 67.3%; Score 37; DB 4; Length 183;
 Best Local Similarity 54.5%; Pred. No. 16;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLTAYAMDY 11
 DB 106 RVSLTAYALDF 116

RESULT 5

Q9NT91 PRELIMINARY; PRT; 190 AA.
 AC Q9NT91;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKFZP434B1722.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]

SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RC Blum H., Bauerachs S., Mewes H.W., Gassenhuber J., Wiemann S.;
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AL137464; CAB70751.1; -

KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 190 AA; 21833 MW; D9C9D7BCDE006CE9 CRC64;

Query Match 67.3%; Score 37; DB 4; Length 190;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVSLTAYAMDY 11
::|||::|
Db 127 KMSLNAYALDF 137

RESULT 6

097CJ6 PRELIMINARY; PRT; 322 AA.
AC 097CJ6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein TV0105.
TV0105 OR TVG0110910.
Thermoplasma volcanium.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN (1)

RP SEQUENCE FROM N.A.
RC STRAIN=SS1 / DSM 4239 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima O-hya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshita T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,
RT "Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium."
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000991; BAB59247.1; -
DR InterPro; IPR002729; DUF48.
DR Pfam; PF01867; DUF48; 1.
DR ProDom; PD008695; DUF48; 1.
DR TIGRFAMs; TIGR00287; TIGR00287; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 322 AA; 37255 MW; 5FB6133DABE746C8 CRC64;

Query Match 67.3%; Score 37; DB 17; Length 322;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVSLTAYAMDY 11
::|||::|
Db 43 KVSLSWALDY 53

RESULT 7

08DVU3 PRELIMINARY; PRT; 387 AA.
AC 08DVU3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN SMU.372.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferreretti J.J.,
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
pathogen."
RT Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

DR EMBL; AE014885; AAN58130.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 387 AA; 45217 MW; 46F6D2F75FE69CE0 CRC64;

Query Match 67.3%; Score 37; DB 16; Length 387;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RVSLTAYAMDY 11
::|||::|
Db 220 RSLTNYTADY 230

RESULT 8

09NXV7 PRELIMINARY; PRT; 391 AA.
AC 09NXV7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ20035.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC Tissue=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Oca T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000042; BA90901.1; -
KW Hypothetical protein.
SQ SEQUENCE 391 AA; 44697 MW; BF9A267A7ED1BA6B CRC64;

Query Match 67.3%; Score 37; DB 4; Length 391;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVSLTAYAMDY 11
::|||::|
Db 314 KMSLNAYALDF 324

RESULT 9

081Y21 PRELIMINARY; PRT; 1712 AA.
AC 081Y21;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ20035.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC Tissue=Brain;
RA Strausberg R.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038115; AAH38115.1; -
KW Hypothetical protein.
SQ SEQUENCE 1712 AA; 197824 MW; ES1D3588135D2066 CRC64;

Query Match 67.3%; Score 37; DB 4; Length 1712;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVSLTAYAMDY 11
::|||::|

Db 1635 KMSLNAYALDF 1645

RESULT 10

08DCL2 PRELIMINARY; PRT; 255 AA.
ID 08DCL2
AC 08DCL2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative salt-induced outer membrane protein.
GN Vv11391.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxId=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Chey H.E.;
"Complete genome sequence of Vibrio vulnificus CMCP6,"
submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016801; AAC09840.1; -
KM Complete proteome.
SQ SEQUENCE 255 AA; 28971 MW; 8ACAB07128790F68 CRC64;

Query Match 65.5%; Score 36; DB 16; Length 255;
Best Local Similarity 88.9%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSILTAYAMD 10
Db 16 VSILTAYAD 24

RESULT 11

0972D4 PRELIMINARY; PRT; 275 AA.
ID 0972D4
AC 0972D4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein Sml194.
GN Sml194.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
NCBI_TaxId=11955;
[1]
SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RA PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sakine M., Baba S.-I., Anai A., Koga H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kusuda N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
"Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7,"
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000985; BAB66235.1; -
DR InterPro; IPR006638; E1p3.1;
DR SMART; SM00729; E1p3.1;
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 275 AA; 32042 MW; 869625BD4F2C3027 CRC64;

Query Match 65.5%; Score 36; DB 17; Length 275;
Best Local Similarity 63.6%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RVSLTAYAMDY 11

Db 22 KVSETAYALOY 32

RESULT 12

0908H7 PRELIMINARY; PRT; 286 AA.
ID 0908H7
AC 0908H7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE M124R.
GN M124R.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxId=31530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lausanne;
RX MEDLINE=20032073; PubMed=10562494;
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macallay C., Miller D., Evans D., McFadden G.;
RT "The complete DNA sequence of myxoma virus."
RL Virology 264:298-318(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Lausanne;
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macallay C., Miller D., Evans D., McFadden G.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170726; AAF15012.1; -
SQ SEQUENCE 286 AA; 32627 MW; 90C638BAE0AF7546 CRC64;

Query Match 65.5%; Score 36; DB 12; Length 286;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVSLTAYAMDY 11
Db 4 RVSVSHVDY 14

RESULT 13

08PKD3 PRELIMINARY; PRT; 369 AA.
ID 08PKD3
AC 08PKD3;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Plasmid-related protein.
GN ORF10 OR XAC2242.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
NCBI_TaxId=92829;
[1]
SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Chiapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madela A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezsa R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparative of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).
 DR EMBL: AE011861; AAM37095.1; -;
 DR InterPro: IPR002226; N12N6_mtfase.
 DR InterPro: IPR002052; N6_Mcase.
 DR InterPro: IPR000051; SAM_bind.
 DR PRINTS: PR00507; N12N6MTRFase.
 DR PROSITE: PS00092; N6_MTASE; 1.
 KW Complete proteome.
 SQ SEQUENCE 369 AA; 40745 MW; 754FD19FA44F84E0 CRC64;
 Query Match 65.5%; Score 36; DB 16; Length 369;
 Best Local Similarity 54.5%; Pred. No. 53;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 1 RVSLTAYAMDY 11
 :|||:|:
 61 RAOVTAYAVEY 71
 RESULT 14
 ID Q9EWT9 PRELIMINARY; PRT; 454 AA.
 AC Q9EWT9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative secreted protease.
 GN SC00732 OR 3SC5B7.10.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 NC NCB1_TaxID=1902;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parikhil J., Barrell B.G., Rajandream M.A.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmid and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21966410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL939106; CAC14934.1; -;
 DR HSP; Pali40; ZSFA.

DR InterPro: IPR004236; AL_protease.
 DR InterPro: IPR001316; Endoprotease2A.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF02983; AL_protease_1.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PRO0861; ALTYICTPASE.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00134; TRYP_SIN_HIS; 1.
 DR PROSITE: PS00135; TRYP_SIN_SER; 1.
 KW Hydrolase; Protease; Serine protease; Complete proteome.
 SQ SEQUENCE 454 AA; 46273 MW; 8708E7726D0DD1D9 CRC64;
 Query Match 65.5%; Score 36; DB 16; Length 454;
 Best Local Similarity 63.6%; Pred. No. 66;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RVSLTAYAMDY 11
 :|||:|:
 DB 119 RVAGTAMALDY 129
 RESULT 15
 ID Q9GUW2 PRELIMINARY; PRT; 145 AA.
 AC Q9GUW2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE C-type lectin TC14-1.
 GN TC14-1.
 OS Polyandrocampa misakiensis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Styelidae; Polyandrocampa.
 NC NCB1_TaxID=7723;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Matsumoto J., Fujiwara S., Yubisui T., Kawamura K.;
 RT "Cytostatic activity of C-type lectins on multipotent epithelial cells
 RT in budding tunicates.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB049563; BAB16304.1; -;
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; lectin_cg_1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 KW Lectin.
 SQ SEQUENCE 145 AA; 16056 MW; 87DAC389C9DCD59D CRC64;
 Query Match 63.6%; Score 35; DB 5; Length 145;
 Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TAYAMDY 11
 :|||:|:
 DB 17 TSYAMDY 23

Search completed: September 10, 2003, 17:42:03
 Job time : 33.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:34:47 ; Search time 11 Seconds
(without alignments)
47.027 Million cell updates/sec

Title: US-09-759-112a-19
Perfect score: 55
Sequence: 1 RVS1TAYAMDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.8	370	1	PNK3_HUMAN	Q9h999 homo sapien
2	61.8	370	1	PNK3_MOUSE	Q8r2w9 mus musculu
3	61.8	388	1	ALR_BACHD	Q9kff9 bacillus ha
4	61.8	599	1	YJUI_YEAST	P32825 saccharomyc
5	61.8	738	1	DHER_ACEPO	P28035 acetobacter
6	61.8	732	1	DHER_ACEBU	Q44002 acetobacter
7	61.8	742	1	DHER_ACEAC	P18278 acetobacter
8	61.8	757	1	DHER_GLUOX	O05542 gluconobact
9	61.8	803	1	DCML_HYDPS	P19913 hydrogenuph
10	61.8	1653	1	YFHM_ECOLI	P76578 escherichia
11	60.0	302	1	YAJF_ECOLI	P23917 escherichia
12	60.0	548	1	PNK1_MOUSE	Q8k4k6 mus musculu
13	60.0	570	1	PNK2_HUMAN	Q9b423 homo sapien
14	60.0	598	1	PNK1_HUMAN	Q8t044 homo sapien
15	60.0	1115	1	DP3A_BACSV	O34623 bacillus su
16	58.2	127	1	GC52_PSEAE	Q91136 pseudomonas
17	58.2	150	1	VLI_HYV67	P50825 human papil
18	58.2	182	1	APT_PSEAE	Q04633 pseudomonas
19	58.2	329	1	MRAV_LACLA	Q9c170 lactococcus
20	58.2	360	1	RFT_PASMU	P57852 pasteurella
21	58.2	490	1	IFT4_HUMAN	O14579 homo sapien
22	58.2	985	1	INVA_YERPS	P11922 yerinia ps
23	58.2	1230	1	UGS4_SOLTU	Q43846 solanum tub
24	56.4	97	1	CMGC_BACLI	Q8v471 bacillus il
25	56.4	134	1	YBIM_ECOLI	P75781 escherichia
26	56.4	185	1	ADH_ANAPL	P30350 anae platyr
27	56.4	189	1	PAAD_NEIMA	Q9j478 neisseria m
28	56.4	189	1	PAAD_NEIMA	Q9j478 neisseria m
29	56.4	268	1	YCT3_HAEIN	P44596 haemophilus
30	56.4	268	1	YCT3_HAEIN	P44596 haemophilus
31	56.4	311	1	PPAC_STRPY	Q9a1a2 streptococc
32	56.4	340	1	OMP2_CHLTR	P38006 chlamydia t
33	56.4	355	1	RFL_CAMJE	Q9p663 campylobact

34	31	56.4	359	1	RFL_BRUME	Q8y195 bruceella me
35	31	56.4	359	1	RFL_RHILLO	Q98993 rhizobium 1
36	31	56.4	360	1	RFL_AGRTS	Q8ub88 agrobacteri
37	31	56.4	360	1	RFL_ECOLI	P07011 escherichia
38	31	56.4	360	1	RFL_RHIME	Q92mk5 rhizobium
39	31	56.4	360	1	RFL_SALTY	P13654 salmoneila
40	31	56.4	360	1	RFL_YERPE	Q8z6x8 yerinia pe
41	31	56.4	361	1	RFL_COXBU	P47849 coxiella bu
42	31	56.4	361	1	RFL_HAEIN	P43917 haemophilus
43	31	56.4	441	1	DHWT_TAXCA	O81169 taxus canad
44	31	56.4	453	1	SYS_ARCFU	O28244 archaeeoglob
45	31	56.4	464	1	GRA3_RAT	P24524 rattus norv

ALIGNMENTS

RESULT 1
ID PNK3_HUMAN STANDARD; PRT; 370 AA.
AC Q9h999;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pantothenate kinase 3 (EC 2.7.1.33) (Pantothenic acid kinase 3)
DE (hpank3).
GN PANK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
ON (1)
RP SEQUENCE FROM N.A.
RA Iisogai T., Ota T., Hayashi K., Sugiyama T., Otaki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takenuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuko Y., Oshima A.,
RT "NEO human cDNA sequencing project";
RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheimen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stamenkovic M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantinck P., Prange C.,
RA Rana S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (3)
RP TISSUE SPECIFICITY.
RX MEDLINE=21372465; PubMed=11479594;
RA Zhou B., Westaway S.K., Levinson B., Johnson M.A., Gitschler J.,
RA Haylick S.J.;
RT "A novel pantothenate kinase gene (PANK2) is defective in
Hallerorden-Spatz syndrome";
RL Nat. Genet. 28:345-349(2001).
CC -!- FUNCTION: Plays a role in the physiological regulation of the

```

CC intracellular CoA concentration (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
CC thioesters (By similarity).
CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Highly expressed in the liver.
CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AK022961; BAB14333.1; -.
CC Genew; HGNC; 19365; PANK3.
CC MIM; 606161; -.
CC InterPro; IPR004567; Pank_eukar.
CC DR Pfam; PF03630; Fumble; 1.
CC KM Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis.
CC SO SEQUENCE 370 AA; 41094 MW; 71EPA56079F352D CRC64;

Query Match 61.8%; Score 34; DB 1; Length 370;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 VSLTAYAMDY 11
Db 331 MKLLAYALDY 340

RESULT 2
PANK3_MOUSE
ID PANK3_MOUSE STANDARD; PRT; 370 AA.
AC QGR2R9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pantothenate kinase 3 (EC 2.7.1.33) (Pantothenic acid kinase 3)
DE (Pank3).
GN PANK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Plangin S.J.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kirywiniski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
```

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Plays a role in the physiological regulation of the
CC intracellular CoA concentration (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
CC thioesters (By similarity).
CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; BC027089; AAH27089.1; -.
CC DR EMBL; BC032188; AAH32188.1; -.
CC DR MGD; MGI:2387464; Pank3.
CC DR InterPro; IPR004567; Pank_eukar.
CC DR Pfam; PF03630; Fumble; 1.
CC KM Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis.
CC SO SEQUENCE 370 AA; 41120 MW; 61D982A619E83A78 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 370;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 VSLTAYAMDY 11
Db 331 MKLLAYALDY 340

RESULT 3
ALR_BACHD
ID ALR_BACHD STANDARD; PRT; 388 AA.
AC QGKFR9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
DE ALR OR BH0520.
GN ALR OR BH0520.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=86665;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RC MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirata C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
```

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CC -----
DR EMBL; AP001508; BAB04239.1; -.
DR PIR; H83714; H83714.
DR HSSP; P10724; 1BD0.
DR HAMAP; MF_01201; -. 1.
DR InterPro; IPR000821; Ala_racemase.
DR Pfam; PF00842; Ala_racemase_C; 1.
DR PRINTS; PRO0992; ALARACEMASE.
DR TIGRfam; TIGR00492; ala; 1.
DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
DR Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
KM Complete proteome.
FT ACT_SITE 40 40 CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
FT ACT_SITE 40 40 SIMILARITY).
FT ACT_SITE 269 269 CATALYTIC BASE SPECIFIC TO L-ALANINE (BY
FT ACT_SITE 269 269 SIMILARITY).
FT BINDING 40 40 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 388 AA; 44020 MW; 8017C15D03C9A66A CRC64;
Query Match 61.8%; Score 34; DB 1; Length 388;
Best Local Similarity 45.5%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RVSLETAAYMDY 11
Db 101 RITLFTVYQLDW 111

RESULT 4
ID YU1 YEAST STANDARD; PRT; 599 AA.
AC P32525;
DT 01-OCT-1993 (rel. 27, Created)
DT 01-FEB-1995 (rel. 31, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Hypothetical 68.5 kDa protein in PRP21-UBP12 intergenic region.
GN YJL201W OR J0325.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycaceae;
OC NCBI_TaxID=4932;
OK [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8288C;
RX MEDLINE=95274326; PubMed=754713;
Purnelle B., Coster P., Goffeau A.;
"The sequence of a 36 kb segment on the left arm of yeast chromosome
X identifies 24 open reading frames including NUC1, PRP21 (SP91),
CDC6, CRV2, the gene for S24, a homologue to the acetylase gene ACO1
and two homologues to chromosome III genes."
RT Yeast 10:1235-1249(1994).
RL [2]
RN SEQUENCE OF 1-323 FROM N.A.
RA MEDLINE=93342071; PubMed=8341697;
Arenas J.E., Abelson J.N.;
"The Saccharomyces cerevisiae PRP21 gene product is an integral
component of the preplisosome."
RT Proc. Natl. Acad. Sci. U.S.A. 90:6771-6775(1993).
RL [1]
CC -1- SIMILARITY: Contains 1 Rho-GAP domain.
CC -----
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CC -----
DR EMBL; X77688; CAA54756.1; -.
DR EMBL; Z49476; CAA89496.1; -.
DR EMBL; L07744; AAB09602.1; -.
DR PIR; S46630; S46630.

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DR SGD; S0003737; ECM25.
DR GO; GO:0007047; P:cell wall organization and biogenesis; IMP.
DR InterPro; IPR000198; RhogAP.
DR SMART; SM00324; RhogAP; 1.
DR PROSITE; PS50238; RHOGAP; 1.
DR Hypothetical protein.
KM DOMAIN 181 359
SQ SEQUENCE 599 AA; 68463 MW; 0A23F564E04597DE CRC64;
Query Match 61.8%; Score 34; DB 1; Length 599;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RVSLETAAYMDY 11
Db 157 RITLFTVYQLDW 167

RESULT 5
ID DHET ACEPO STANDARD; PRT; 738 AA.
AC P28036;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-AUG-1992 (rel. 23, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Alcohol dehydrogenase [acceptor] precursor (EC 1.1.99.8).
GN ADHA.
OS Acetobacter polyxogenes.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.
OK NCBI_TaxID=439;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=NB11028;
RX MEDLINE=91159482; PubMed=2001402;
Tamura T., Fukaya M., Takemura H., Tayama K., Okumura H.,
Kawamuta Y., Nishiyama M., Horinouchi S., Beppu T.;
"Cloning and sequencing of the gene cluster encoding two subunits of
membrane-bound alcohol dehydrogenase from Acetobacter polyxogenes."
RT Biochim. Biophys. Acta 1088:297-300(1991).
RL Biochim. Biophys. Acta 1088:297-300(1991).
CC -1- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPT: METHANOL).
CC -1- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde +
CC reduced acceptor.
CC -1- COFACTOR: PO4 AND HEME.
CC -1- SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND TWO
CC SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDROGENASE
CC COMPLEX.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC
CC SPACE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
CC -1- SIMILARITY: Contains 1 cytochrome c domain.
CC -----
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CC -----
DR EMBL; D00635; BAA00528.1; -.
DR PIR; S14270; S14270.
DR HSSP; 09247; 1PLG.
DR InterPro; IPR001479; Bac_POQ.
DR InterPro; IPR002372; Bac_POQ_repeat.
DR Pfam; PF01011; Bacterial_POQ; 3.
DR SMART; SM00564; POQ; 3.
DR PROSITE; PS00363; BACTERIAL_POQ_1; 1.
DR PROSITE; PS00364; BACTERIAL_POQ_2; 1.
DR PROSITE; PS00190; CYTOCHROME_C_1.
DR Oxidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.
FT SIGNAL 1 35

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FT CHAIN 36 738 ALCOHOL DEHYDROGENASE [ACCEPTOR].
 FT DOMAIN 634 738 CYTOCHROME C-LIKE.
 FT BINDING 650 650 HEME (COVALENT) (BY SIMILARITY).
 FT BINDING 653 653 HEME (COVALENT) (BY SIMILARITY).
 FT METAL 654 654 IRON (HEMEXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 738 AA; 80840 MW; 1E2BED7BCD92AF6 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 738;
 Best Local Similarity 70.0%; Pred. No. 39;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTYAMD 10
 DB 685 RGALTAYGMD 694

RESULT 6
 DHET_ACEU STANDARD; PRT; 739 AA.

Q44002; 007952;
 15-DEC-1998 (Rel. 37, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alcohol dehydrogenase [acceptor] precursor (EC 1.1.99.8).
 GN ADH.
 OS Acetobacter europaeus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Acetobacteraceae; Gluconacetobacter.
 NCBI_TaxID=33995;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=DES1 / DSM 6160;
 RA Thurner C.A.K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde +
 reduced acceptor.
 CC -1- COFACTOR: POQ AND HEME (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND TWO
 SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDROGENASE
 COMPLEX (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC
 SPACE (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
 CC -1- SIMILARITY: Contains 1 cytochrome c domain.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X82894; CAAS8066.1; -
 DR EMBL; Y09480; CAA70688.1; -
 DR HSSP; Q924J7; 1FLG.
 DR InterPro; IPR001479; Bac_POQ.
 DR InterPro; IPR002372; Bac_POQ_repeat.
 DR InterPro; IPR000345; CytC_heme_bind.
 DR Pfam; PF01011; Bacterial_POQ_3.
 DR SMART; SM00564; POQ_3.
 DR PROSITE; PS00363; BACTERIAL_POQ_1; 1.
 DR PROSITE; PS00364; BACTERIAL_POQ_2; 1.
 DR PROSITE; PS00190; CYTOCHROME_C_1.
 DR Oxidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.
 KM Oxidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.
 FT SIGNAL 1 35
 FT CHAIN 36 739 ALCOHOL DEHYDROGENASE [ACCEPTOR].
 FT DOMAIN 635 739 CYTOCHROME C-LIKE.
 FT BINDING 651 651 HEME (COVALENT) (BY SIMILARITY).
 FT BINDING 654 654 HEME (COVALENT) (BY SIMILARITY).
 FT METAL 655 655 IRON (HEMEXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 739 AA; 80944 MW; E681BB237ACB91F4 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 739;
 Best Local Similarity 70.0%; Pred. No. 39;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTYAMD 10
 DB 686 RGALTAYGMD 695

RESULT 7

DHET_ACEAC STANDARD; PRT; 742 AA.

AC P18278;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alcohol dehydrogenase [acceptor] precursor (EC 1.1.99.8).
 GN ADHA OR ADH1.
 OS Acetobacter aceti.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Acetobacteraceae; Acetobacter.
 NCBI_TaxID=435;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 36-50.
 RX MEDLINE=89255070; PubMed=2722742;
 RA Inoue T., Sunagawa M., Mori A., Imai C., Fukuda M., Takagi M.,
 RA Yano K.;
 RL "Cloning and sequencing of the gene encoding the 72-kilodalton
 dehydrogenase subunit of alcohol dehydrogenase from Acetobacter
 aceti.";
 RL J. Bacteriol. 171:3115-3122(1989).
 RN (2)
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=9528964; PubMed=7772016;
 RA Cozier G.E., Giles I.G., Anthony C.;
 RT "The structure of the quinoprotein alcohol dehydrogenase of
 Acetobacter aceti modelled on that of methanol dehydrogenase from
 Methylobacterium extorquens.";
 RL Biochem. J. 308:375-379(1995).
 CC -1- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde +
 reduced acceptor.
 CC -1- COFACTOR: POQ AND HEME.
 CC -1- SUBUNIT: TETRAMER OF NON IDENTICAL CHAINS (DEHYDROGENASE,
 CYTOCHROME, AND TWO SMALLER UNKNOWN SUBUNITS).
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
 CC -1- SIMILARITY: Contains 1 cytochrome c domain.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D90004; BAA14058.1; -
 DR PIR; J50326; J50326.
 DR HSSP; Q924J7; 1FLG.
 DR InterPro; IPR001479; Bac_POQ.
 DR InterPro; IPR002372; Bac_POQ_repeat.
 DR InterPro; IPR000345; CytC_heme_bind.
 DR Pfam; PF01011; Bacterial_POQ_3.
 DR SMART; SM00564; POQ_3.
 DR PROSITE; PS00363; BACTERIAL_POQ_1; 1.
 DR PROSITE; PS00364; BACTERIAL_POQ_2; 1.
 DR PROSITE; PS00190; CYTOCHROME_C_1.
 DR Oxidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.
 KM Oxidoreductase; POQ; Heme; Periplasmic; Membrane; Signal.
 FT SIGNAL 1 35
 FT CHAIN 36 742 ALCOHOL DEHYDROGENASE [ACCEPTOR].
 FT DOMAIN 633 742 CYTOCHROME C-LIKE.
 FT ACT SITE 343 343 BASE (POTENTIAL).
 FT BINDING 649 649 HEME (COVALENT) (BY SIMILARITY).

FT BINDING 652 652 HEME (COVALENT) (BY SIMILARITY).
FT METAL 653 653 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 742 AA; 81521 MW; 9C6C9268DABB825A CRC64;
Query Match 61.8%; Score 34; DB 1; Length 742;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RVSLTAYAMD 10
Db 684 RGALTRAYGMD 693
RESULT 8
DHET GLUTOX STANDARD; PRT; 757 AA.
AC 005542;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alcohol dehydrogenase [acceptor] precursor (EC 1.1.99.8) (G3-ADH subunit I).
GN ADHA.
OS Gluconobacter oxydans (Gluconobacter suboxydans).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconobacter.
OX NCBI_TaxID=442;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 36-50.
RC STRAIN=IFO 12528; PubMed=9055427;
RA MEDLINE=97208225; PubMed=9055427;
RX Kondo K., Horinouchi S.;
RT "Characterization of the genes encoding the three-component membrane-bound alcohol dehydrogenase from Gluconobacter suboxydans and their expression in Acetobacter pasteurianus".
RL Appl. Environ. Microbiol. 63:1131-1138(1997).
CC -1- FUNCTION: DEHYDRATION OF PRIMARY ALCOHOLS (EXCEPTION: METHANOL) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: A primary alcohol + acceptor = an aldehyde + reduced acceptor.
CC -1- COFACTOR: POQ AND HEME.
CC -1- SUBUNIT: HETEROTRIMER (DEHYDROGENASE, CYTOCHROME AND PROTEIN ADHS), THAT FORMS THE ALCOHOL DEHYDROGENASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC SPACE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
CC -1- SIMILARITY: contains 1 cytochrome c domain.

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DR EMBL: D86375; BAA19753.1; -
DR HSSP: Q9Z4J7; 1F1G.
DR InterPro: IPR001479; Bac_POQ.
DR InterPro: IPR002372; Bac_POQ_repeat.
DR InterPro: IPR000345; CytC_heme_bind.
DR Pfam: PF01011; Bacterial_POQ_4.
DR SMART: SM00564; POQ; 6.
DR PROSITE: PS00363; BACTERIAL_POQ_1; 1.
DR PROSITE: PS00364; BACTERIAL_POQ_2; 1.
DR PROSITE: PS00190; CYTOCHROME_C_1.
DR Oxidoreductase; POQ; Heme; Periplasmic; Membrane; signal;
KW Pyridoxaldehyde carboxylic acid.
FT SIGNAL 1 34
FT CHAIN 35 757 ALCOHOL DEHYDROGENASE [ACCEPTOR].
FT DOMAIN 637 726 CYTOCHROME C-LIKE.
FT MOD_RES 35 35 PYRIDOXINE CARBOXYLIC ACID.
FT ACT_SITE 342 342 BASE (POTENTIAL).

FT BINDING 653 653 HEME (COVALENT) (BY SIMILARITY).
FT METAL 656 656 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 757 AA; 82968 MW; 39B9F03EB3947581 CRC64;
Query Match 61.8%; Score 34; DB 1; Length 757;
Best Local Similarity 70.0%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RVSLTAYAMD 10
Db 688 RGALTRAYGMD 697
RESULT 9
DCML HYDPS STANDARD; PRT; 803 AA.
ID DCML_HYDPS Q9RBR9;
AC P1913; Q9RBR9;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L).
GN CUTH.
OS Hydrogenophaga pseudoflava (Pseudomonas carboxydoflava).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Hydrogenophaga.
OX NCBI_TaxID=47421;
RN [1]
RP SEQUENCE FROM N.A., COFACTOR, AND SUBUNIT.
RA MEDLINE=99412255; PubMed=10482497;
RX Kang B.S., Kim Y.M.;
RT "Cloning and molecular characterization of the genes for carbon monoxide dehydrogenase and localization of molybdenum, flavin adenine dinucleotide, and iron-sulfur centers in the enzyme of Hydrogenophaga pseudoflava".
RL J. Bacteriol. 181:5581-5590(1999).
RN [2]
RP SEQUENCE OF 1-9.
RX MEDLINE=9005678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in carboxydophilic bacteria".
RL Arch. Microbiol. 152:335-341(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
RX MEDLINE=20425113; PubMed=10966817;
RA Haenzelmann P., Dobbek H., Gremer L., Huber R., Meyer O.;
RT "The effect of intracellular molybdenum in Hydrogenophaga pseudoflava on the crystallographic structure of the seleno-molybdo-iron-sulfur flavoenzyme carbon monoxide dehydrogenase".
RL J. Mol. Biol. 301:1221-1235(2000).
RN [4]
RP REVIEW.
RX MEDLINE=20525277; PubMed=11076018;
RA Meyer O., Gremer L., Ferner R., Dobbek H., Gnida M., Meyer-Klaucke W., Huber R.;
RT "The role of Se, Mo and Fe in the structure and function of carbon monoxide dehydrogenase".
RL Biol. Chem. 381:865-876(2000).
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor.
CC -1- COFACTOR: Molybdenum (molybdopterin).
CC -1- SUBUNIT: COMPOSED OF 2 HETEROTRIMERS. EACH HETEROTRIMER CONSISTS OF A LARGE, A MEDIUM AND A SMALL SUBUNIT. THE HETEROTRIMERS DIMERIZE TO FORM A HEXAMER.

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CC
 DR EMBL; U0806; AAD00363.1; -
 DR PIR; P10139; P10139.
 DR PDB; 1FEV; 15-SEP-00.
 DR PDB; 1FEV; 13-NOV-00.
 DR Pfam; PF02738; Ald_Xan_dh_C2; 1.
 DR Pfam; PF01315; Ald_Xan_dh_C; 1.
 KM Oxidoreductase; Molybdenum; Selenium; Selenocysteine; 3D-structure.
 SE CDS 385 385
 SQ SEQUENCE 803 AA; 87228 MW; 3CD5FE205DBE0712 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 803;
 Best Local Similarity 60.0%; Pred. No. 42;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSLTAYVAMDY 11
 : ||| :
 302 ISTTAFARDY 311

RESULT 10
 ID YFHM_ECOLI STANDARD; PRT; 1653 AA.
 AC P76578;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Hypothetical lipoprotein yfhm precursor.
 GN YFHM OR B2520.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 Science 277:1453-1474(1997).
 RL -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Potential).

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CC
 DR EMBL; AE000338; AAC75573.1; -
 DR PIR; G65028; G65028.
 DR Ecogen; EG1394; yfhm.
 DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
 KM Hypothetical protein; Membrane; Lipoprotein; Signal; Coiled coil;
 KM Complete proteome.
 FT CHAIN 1 17 POTENTIAL.
 FT SIGNAL 1 17
 FT DOMAIN 18 1653 HYPOTHETICAL LIPOPROTEIN YFHM.
 FT LIPID 18 1559 COILED COIL (POTENTIAL).
 FT LIPID 18 1589 N-ACYL DIGLYCERIDE (POTENTIAL).
 SQ SEQUENCE 1653 AA; 181584 MW; 13109EC5CDEBA1A0 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 1653;
 Best Local Similarity 75.0%; Pred. No. 91;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTVAYMDY 11
 |||| :
 Db 1253 LTVAYWDF 1260

RESULT 11
 ID YAJF_ECOLI STANDARD; PRT; 302 AA.
 AC P23917; P71316; P75705;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yajf.
 GN YAJF OR B0394.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Ryder L., Sharples G.J., Lloyd R.G.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 Science 277:1453-1474(1997).
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
 RA Federspiel N., Hyman R., Kaiman S., Komp C., Kundi O., Lew H.,
 RA Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 43-302 FROM N.A.
 RX MEDLINE=92078081; PubMed=1744033;
 RA Reeder T.C., Schleif R.F.;
 RT "Mapping, sequence, and apparent lack of function of araJ, a gene of
 RT the Escherichia coli arabinose regulon.";
 J. Bacteriol. 173:7765-7771(1991).
 RL J. Bacteriol. 173:7765-7771(1991).
 CC -1- SIMILARITY: BELONGS TO THE ROK (NAGC/XYLR) FAMILY. STRONG, TO
 CC H. INFLUENZAE HI0182.

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CC
 DR EMBL; X76979; CAA54284.1; -
 DR EMBL; AE000145; AAC73497.1; ALT_INIT.
 DR EMBL; U73857; AAB18118.1; ALT_INIT.
 DR EMBL; M64787; AAA23475.1; -
 DR PIR; B64768; B64768.
 DR Ecogen; EG1288; yajf.
 DR InterPro; IPR000600; ROK_family.
 DR Pfam; PF00480; ROK; 1.
 DR PROSITE; PS0125; ROK; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 302 AA; 32500 MW; 9791F9C29C91049C CRC64;

Query Match 60.0%; Score 33; DB 1; Length 302;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSITAYAMDY 11
 DB 188 ISCTGFAMDY 197

RESULT 12
 ID PANK1_MOUSE STANDARD; PRT; 548 AA.
 AC Q8K4K6; Q9D3K1, Q9QXW8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic acid kinase 1)
 GN (mpank1) (mpank).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;

(1)
 SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
 MEDLINE=20092916; PubMed=10625688;
 Rock C.O., Calder R.B., Karim M.A., Jackowski S.;
 "Pantothenate kinase regulation of the intracellular concentration of
 coenzyme A.";
 J. Biol. Chem. 275:1377-1383(2000).
 (2)
 SEQUENCE FROM N.A. (ISOFORM 1), CHARACTERIZATION, AND ALTERNATIVE
 SPLICING.
 MEDLINE=22090536; PubMed=12095677;
 Rock C.O., Karim M.A., Zhang Y.M., Jackowski S.;
 "The murine pantothenate kinase (Pank1) gene encodes two
 differentially regulated pantothenate kinase isozymes.";
 Gene 291:35-43(2002).
 (3)
 SEQUENCE FROM N.A. (ISOFORM 1).
 STRAIN=C57BL/6J; TISSUE=Heart;
 MEDLINE=21085660; PubMed=1217851;
 Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Glasl C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Batsch G.,
 Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Guenichon S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Norioka P., Ring B., Rindowbach C., Seta T., Shizata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
 Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection.";
 Nature 409:685-690(2001).
 (4)
 SEQUENCE FROM N.A. (ISOFORM 2).
 TISSUE=Liver, and Skeletal muscle;
 MEDLINE=22388257; PubMed=12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Umedin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Keltman M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL FUNCTION: Plays a role in the physiological regulation of the
 intracellular CoA concentration.
 CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
 phosphopantothenate.
 CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
 thioesters. Strongly inhibited by acetyl-CoA and by many CoA and
 also inhibited by high concentration of non-esterified CoA
 (CoASH). Isoform 1 is inhibited by high concentration of non-
 esterified CoA (CoASH) and strongly inhibited by acetyl-CoA and by
 malonyl-CoA. Isoform 2 is stimulated by CoA and weakly inhibited
 by acetyl-CoA and malonyl-CoA.
 CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Pank1-alpha;
 CC IsoId=Q8K4K6-1; Sequence=Displayed;
 CC Name=2; Synonyms=Pank1-beta;
 CC IsoId=Q8K4K6-2; Sequence=VSP 004522, VSP 004523;
 CC -1- TISSUE SPECIFICITY: Expressed in liver and kidney. Isoform 1 is
 highly expressed in heart and skeletal muscle, whereas isoform 2
 is expressed exclusively in testis.
 CC -1- DOMAIN: The N-terminal extension, present in isoform 1 may be the
 regulatory domain.
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF200357; AAF2952.1; -
 CC EMBL; AF347700; AAM7216.1; -
 CC EMBL; AK017345; BAB30700.1; -
 CC EMBL; BC023466; AAH23496.1; -
 CC MGD; MGI:192285; Pank1.
 CC GO; GO:0004594; F:pantothenate kinase activity; IDA.
 CC InterPro; IPR004567; Pank_eukar.
 CC Pfam; PF03630; Pumble; 1.
 CC Transferrase; Kinase; ATP-binding; Coenzyme A biosynthesis;
 KW Alternative splicing
 FT VARSPLIC 1 175 Missing (in isoform 2).
 FT /FTId=VSP 004522.
 FT VARSPLIC 176 185 MDSGRKNRP -> MKLVNGRQQT (in isoform 2).
 FT /FTId=VSP 004523.
 FT SEQUENCE 548 AA; 60091 MW; C916709D048E829B CRC64;

QY 2 VSITAYAMDY 11
 DB 506 MKLAVAMDY 515

RESULT 13
 ID PANK2_HUMAN STANDARD; PRT; 570 AA.
 AC Q9BZ23; Q8N7Q4, Q8TCR5, Q9BYW5, Q9HAF2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

Query Match 60.0%; Score 33; DB 1; Length 548;
 Best Local Similarity 60.0%; Pred. No. 46;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE Pantothenate kinase 2, mitochondrial precursor (EC 2.7.1.33)
 DE (Pantothenic acid kinase 2) (hPANK2).
 GN PANK2 OR C20ORF48.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SUBCELLULAR LOCATION.
 RC TISSUE=Brain;
 RX PubMed=12554685;
 RA Hoernagel K., Prokisch H., Meltinger T.;
 RT "An isoform of hPANK2, deficient in pantothenate kinase-associated
 RT neurodegeneration, localizes to mitochondria.";
 RL Hum. Mol. Genet. 12:321-327(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.W., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Cowley G.J., Dedman R., Dhali P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond D.V., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.M., Lawlor S.,
 RA Levesitho M.H., Leverhulme M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McComachie L.J., McLay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Millikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showken R., Sims S.,
 RA Ruce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.W.,
 RA Whithead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmink L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND VARIANT GLY-126.
 RC TISSUE=Testis;
 RA Suzuki O., Sasaki N., Aoeuka S., Shoji T., Ichihara T., Shiohata N.,
 RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
 RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
 RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Katoka R.,
 RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
 RA Matsunabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
 RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kikuma K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
 RA Kikuchi H., Kanda K., Wagaizuma M., Murakawa K., Kanehori K.,
 RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T., Ota T.,
 RA Hayashi K., Hara H., Tanase T., Nomura Y., Togiya S., Komai F.,
 RA Hara R., Takeuchi K., Arita M., Nabekura T., Kawai Y.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 406-570 FROM N.A.
 RC TISSUE=Brain;
 RA Koehler K., Beyer A., Mewes H.-W., Weil B., Wiemann S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP DISEASE.
 RX MEDLINE=22053542; PubMed=12058097;
 RA Ching K.H.L., Westaway S.K., Gitschier J., Higgins J.J.,

RA Hayflick S.J.;
 RT "HAP syndrome is allelic with pantothenate kinase-associated
 RT neurodegeneration.";
 RL Neurology 58:1673-1674(2002).
 RN [6]
 RP VARIANTS GLN-111 AND GLY-126, VARIANTS PRAN VAL-219; ALA-234; TRP-264;
 RP CYS-278; VAL-282; CYS-286; ILE-327; PRO-351; SER-355; ILE-404;
 RP PRO-413; ASN-471; THR-497; ILE-500; ARG-521 AND MET-528, AND TISSUE
 RP SPECIFICITY.
 RX MEDLINE=21372465; PubMed=11479594;
 RA Zhou B., Westaway S.K., Levinson B., Johnson M.A., Gitschier J.,
 RA Hayflick S.J.;
 RT "A novel pantothenate kinase gene (PANK2) is defective in
 RT Hallervorden-Spatz syndrome.";
 RL Nat. Genet. 28:345-349(2001).
 CC -1- FUNCTION: Maybe the master regulator of the CoA biosynthesis (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
 CC phosphopantothenate.
 CC -1- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
 CC thioesters.
 CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and mitochondrial.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9B23-1; Sequence=Displayed;
 CC Note=Mitochondrial isoform;
 CC Name=3;
 CC IsoId=Q9B23-2; Sequence=VSP_007424;
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, 1 (shown here) and 2, are produced by
 CC alternative initiation;
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- DISEASE: Defects in PANK2 are the cause of pantothenate kinase-
 CC associated neurodegeneration (PKAN) [MIM:234200], formerly known
 CC as Hallervorden-Spatz syndrome (HSS). PKAN is an autosomal
 CC recessive neurodegenerative disorder associated with iron
 CC accumulation in the brain. Clinical features include
 CC extrapyramidal dysfunction, and a relentlessly progressive course.
 CC Atypical PKAN is diagnosed in individuals who may not fit with the
 CC diagnostic criteria of PKAN yet have radiographic or pathologic
 CC evidence of increased basal ganglia iron.
 CC -1- DISEASE: Defects in PANK2 are the cause of
 CC hypoparathyroidism, acanthocytosis, retinitis pigmentosa,
 CC and pallidal degeneration (HARP) [MIM:607236]. HARP is a rare
 CC syndrome with many clinical similarities to PKAN.
 CC -1- MISCELLANEOUS: The HSS syndrome has been proposed to
 CC and Hugo Spatz during World War II.
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -1- CAUTION: In addition to the presence of a second start site in
 CC position 124, it is not excluded that the Leu-111 may
 CC exceptionally also serve as an alternative initiation codon.
 CC -----
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 CC -----
 CC EMBL; AF944409; AAN32907.1; -;
 CC EMBL; AL353194; CAC15924.2; ALT_SEQ.
 CC EMBL; AL031670; CAC32829.1; -;
 CC EMBL; AK021791; BAB13897.1; -;
 CC EMBL; AK097796; BAC05173.1; ALT_INIT.
 CC EMBL; AL713654; CAD28463.1; -;
 CC Genew; HGNC:15894; PANK2.
 CC MIM; 606157; -;

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DR MIM; 234200; -
DR MIM; 607236; -
DR InterPro; IPRO004567; Pank_eukar.
DR Pfam; PF03630; Fumble; 1.
KW Transferrase; kinase; ATP-binding; Coenzyme A biosynthesis;
KW Alternative splicing; Alternative initiation; Transic peptide;
KW Disease mutation; Polymorphism.
FT TRANSIT 1 46 MITOCHONDRION (POTENTIAL).
FT CHAIN 47 570 PANTOTHENATE KINASE 2, ISOFORM 1.
FT INIT MET 124 570 PANTOTHENATE KINASE 2, ISOFORM 2.
FT DOMAIN 236 243 FOR ISOFORM 2.
FT VARSPLIC 1 291 POLY-GLU.
FT VARIANT 111 111 Missing (in isoform 3).
FT VARIANT 126 126 /FTid=VSP_007424.
FT VARIANT 126 126 L -> O.
FT VARIANT 219 219 /FTid=VAR_015152.
FT VARIANT 219 219 A -> G.
FT VARIANT 234 234 /FTid=VAR_015153.
FT VARIANT 234 234 G -> V (in PRAN; atypical).
FT VARIANT 264 264 /FTid=VAR_015154.
FT VARIANT 264 264 T -> A (in PRAN; atypical).
FT VARIANT 264 264 /FTid=VAR_015155.
FT VARIANT 264 264 R -> W (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015156.
FT VARIANT 264 264 R -> C (in PRAN; atypical).
FT VARIANT 264 264 L -> V (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015157.
FT VARIANT 264 264 /FTid=VAR_015158.
FT VARIANT 264 264 R -> C (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015159.
FT VARIANT 264 264 T -> I (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015160.
FT VARIANT 264 264 S -> P (in PRAN; atypical).
FT VARIANT 264 264 /FTid=VAR_015161.
FT VARIANT 264 264 N -> S (in PRAN; atypical).
FT VARIANT 264 264 /FTid=VAR_015162.
FT VARIANT 264 264 N -> I (in PRAN; atypical).
FT VARIANT 264 264 L -> P (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015163.
FT VARIANT 264 264 L -> N (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015164.
FT VARIANT 264 264 S -> N (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015165.
FT VARIANT 264 264 I -> T (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015166.
FT VARIANT 264 264 N -> I (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015167.
FT VARIANT 264 264 G -> R (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015168.
FT VARIANT 264 264 T -> M (in PRAN).
FT VARIANT 264 264 /FTid=VAR_015169.

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Query Match 60.0%; Score 33; DB 1; Length 570;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 4 LTYVANDY 11
DB 533 LAYALDY 540

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RESULT 14
PANK1 HUMAN STANDARD; PRT; 598 AA.
AC 08TE04; 08TE08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic acid kinase 1)
DE (hPank1) (hPank).
GN PANK1 OR PANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Fetal brain;
RX MEDLINE=2168246; PubMed=11809413;
RA Ni X., Ma Y., Cheng H., Jiang M., Ying K., Xie Y., Mao Y.;
RT "Cloning and characterization of a novel human pantothenate kinase
gene."
RL Int. J. Biochem. Cell Biol. 34:109-115(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 460-598 FROM N.A. (ISOFORM 2).
RC TISSUE=Skeletal muscle;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usetin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP IDENTIFICATION OF ISOFORM 1.
RA Zhou B., Westway S.K., Levinson B., Johnson M.A., Gitschler J.,
RA Haylick S.J.;
RL Unpublished observations (JUL-2001).
CC -I- FUNCTION: Plays a role in the physiological regulation of the
intracellular CoA concentration (By similarity).
CC -I- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
phosphopantothenate.
CC -I- ENZYME REGULATION: Regulated by feedback inhibition by CoA and its
thioesters. Strongly inhibited by acetyl-CoA and by many CoA and
also inhibited by high concentration of non-esterified CoA (CoASH)
(By similarity).
CC -I- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -I- ALTERNATIVE PRODUCTS:
CC Name=1; Synonyms=Pank1-alpha;
CC IsoId=Q8TE04-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8TE04-2; Sequence=VSP_004520;
CC Name=3;
CC IsoId=Q8TE04-3; Sequence=VSP_004520, VSP_004521;
CC -I- TISSUE SPECIFICITY: Expressed in liver and kidney.
CC -I- DOMAIN: The N-terminal extension, present in isoform 1 may be the
regulatory domain.
CC -I- SIMILARITY: BELONGS TO THE EUKARYOTIC PANTOTHENATE KINASE FAMILY.
CC -I- CAUTION: Isoform 2, although confirmed in the murine ortholog, is
only partially cloned and needs a further complete identification.
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CC -----
DR EMBL: AF355198; AAL86371.1;
DR EMBL: AL157400; -; NOT ANNOTATED CDS.
DR EMBL: BC026296; AAH26256.1; ALT_INT.
DR EMBL: BK000008; DAA00002.1;
DR GenBank: HGNC:8598; PANK1.
DR MIM: 606160;
DR InterPro: IPR004567; Pank_eukar.
DR Pfam: PF03630; Fumbl; 1.
KM Transferase: Kinase; ATP-binding; Coenzyme A biosynthesis;
KM Alternative splicing.
FT VARSPLIC 1 235
FT MLKLVGGGQDMACVAGTSLGGEAAFEVAPRGQKAG
FT AGSPGMCAGIPDAPAGVLOAGVAPRGQGAEEVGS
FT AGGGEERVRHPPDAPALRLNRKQGSGEIKTPENDLQAG
FT RLSRGPTAPAPQMGDRSGQSRVSHSGAPVTSAAV
FT NGLIHNGFHPVPQPHVCSRGVSGSDAPQLPLPELO
FT POPLPHQDSPAKCKRLRRMDSGRKRRPP -> MKLINKK
FT KQT (in isoform 2 and isoform 3).
FT /Frid=VSP_004520.
FT /Frid=VSP_004521.
FT /Frid=VSP_004521.
SQ VARSPLIC 438 496
SQ CONFLICT 306 306 N -> D (IN REF. 1).
SQ SEQUENCE 598 AA; 64339 MW; 0A92115D5BEDFC4C CRC64;
Query Match 60.0%; Score 33; DB 1; Length 598;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 VSITAYAMDY 11
DB 556 MKLLAYAMDY 565
RESULT 15
DP3A_BACSU STANDARD; PRT; 1115 AA.
AC 034623;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III alpha subunit (EC 2.7.7.7).
GN DNAE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=168;
RP MEDLINE=98048467; PubMed=9387221;
RP Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RP "Sequencing and functional annotation of the Bacillus subtilis genes
RP in the 200 kb rnaB-dnaB region";
RP Microbiology 143:3431-3441(1997).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=168;
RP MEDLINE=98044033; PubMed=9384377;
RP Aenevo V., Bertero M.G., Bessieres P., Bolotin A., Borhett S.,
RP Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RP Brouillet S., Brusch C.V., Caldwell B., Capuano V.J., Carter N.M.,
RP Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RP Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RP Entian K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
RP Fritz C., Fujita M., Fujita Y., Funa S., Gallizi A., Galleron N.,
RP Gilm S.Y., Glaeser P., Goitreau A., Golightly E.J., Grandi G.,
RP Giuseppe G., Guy B.J., Haga K., Haele J., Harwood C.R., Hanaut A.,
RP Hilbert H., Holstappel S., Hosono S., Hullo M.P., Itaya M., Jones L.,
RP Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RP Kobayashi Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
RP Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RP Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

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RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Pario V., Pohl T.M., Portetle D., Porwolik S., Prescott A.M.,
RA Prescan E., Pujić P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
RA Rieger M., Rivolet C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serrit P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takakoshi A., Tanaka T., Terpsstra P., Tognoni A.,
RA Totsuo V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambitt R., Wedler E., Wedler H., Weizenecker T., Jata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Jata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256 (1997).
CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + [DNA] (N).
CC -1- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
CC epsilon and theta chains) that associates with a tau subunit. This
CC core dimerizes to form the POLIT' complex. POLIT' associates
CC with the gamma complex (composed of gamma, delta, delta', psi and
CC chi chains) and with the beta chain to form the complete DNA
CC polymerase III complex (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. DNAE
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: AF008220; AAC00338.1;
DR EMBL: Z29118; CAB14883.1;
DR PIR: D69617; D69617.
DR Subtilist; BG12583; dnaE.
DR InterPro: IPR004013; PHP_C.
DR InterPro: IPR003141; PHP_N.
DR InterPro: IPR004805; POLC_alpha.
DR InterPro: IPR004365; CRNA_anti.
DR InterPro: IPR02811; PHP_C; 1.
DR Pfam: PF02231; PHP_N; 1.
DR Pfam: PF01336; CRNA_anti; 1.
DR SMART: SM00481; POLITIC; 1.
DR TIGRfam: TIGR00594; polc; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW Complete proteome.
SQ SEQUENCE 1115 AA; 125349 MW; E8B04E3398BE512PE CRC64;
OY 2 VSITAYAMDY 11
DB 516 IYITQYAMDH 525

```

Search completed: September 10, 2003, 17:40:52
Job time: 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:38:22 ; Search time 14.85 Seconds
(without alignments)
71.236 Million cell updates/sec

Title: US-09-759-112a-19
Perfect score: 55
Sequence: 1 RVSLTRYAMDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues
number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	69.1	106	2 S26315	Ig heavy chain V r
2	38	69.1	1644	2 AC0823	probable lipoprote
3	37	67.3	190	2 T46408	hypothetical prote
4	35	63.6	345	2 T35266	probable oxidoredu
5	34	61.8	314	2 G96020	conserved hypochet
6	34	61.8	388	2 H83714	alanine racemase B
7	34	61.8	599	2 S46630	hypothetical prote
8	34	61.8	738	2 S14270	alcohol dehydrogen
9	34	61.8	742	2 US0326	alcohol dehydrogen
10	34	61.8	742	2 A49340	alcohol dehydrogen
11	34	61.8	1653	2 B91052	hypothetical prote
12	34	61.8	1653	2 B95896	hypothetical prote
13	34	61.8	1653	2 G65028	hypothetical prote
14	33	60.0	118	2 S32786	Ig heavy chain (an
15	33	60.0	119	2 B53285	Ig heavy chain V a
16	33	60.0	136	2 S04576	Ig heavy chain pre
17	33	60.0	141	2 S52446	Ig heavy chain V r
18	33	60.0	148	2 T51279	ribosomal protein,
19	33	60.0	249	2 AG3076	hypothetical prote
20	33	60.0	249	2 B98210	glutamate/aspartat
21	33	60.0	293	2 T37227	probable sugar tra
22	33	60.0	348	2 B64768	yaif protein - Esc
23	33	60.0	915	2 T19692	hypothetical prote
24	33	60.0	1115	2 D69617	DNA polymerase III
25	32	58.2	15	2 PH1631	Ig H chain V-D-J r
26	32	58.2	119	2 A53285	Ig heavy chain V a
27	32	58.2	127	2 B83339	glycine cleavage s
28	32	58.2	182	2 F83453	adenine phosphorib
29	32	58.2	198	2 AF1870	hypothetical prote

30	32	58.2	289	2 B69217	hypothetical prote
31	32	58.2	329	2 D86733	hypothetical prote
32	32	58.2	334	2 A41497	transcription regu
33	32	58.2	334	2 A11139	transcription regu
34	32	58.2	454	2 T50193	probable seryl-trn
35	32	58.2	480	2 B90012	hypothetical prote
36	32	58.2	519	2 AB3449	xanthine dehydroge
37	32	58.2	531	2 B83422	probable serine/th
38	32	58.2	676	2 E72662	hypothetical prote
39	32	58.2	944	2 S69679	hypothetical prote
40	32	58.2	986	1 A28646	invasin - Yersinia
41	32	58.2	1025	2 H86250	hypothetical prote
42	32	58.2	1048	2 T18334	icmB protein - Leg
43	32	58.2	1230	2 T07663	soluble starch syn
44	31	56.4	111	2 PH0992	Ig heavy chain V r
45	31	56.4	134	2 F64817	probable membrane

ALIGNMENTS

RESULT 1

S26315
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26315
R:Stark, S.E.; Caton, A.U.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <STA>
A:Cross-references: EMBL:X59208; NID:952079; PIDN:CAA41918.1; PID:G1334042
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 38; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAYAMDY 11
Db 89 TAYAMDY 95

RESULT 2

AC0823
probable lipoprotein STY2778 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0823
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Connor, T.; Cornhill, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Mouton, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0823
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1644 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02735.1; PID:G16503746; GSPDB:GN00176
C:Genetics:
A:Gene: STY2778

Query Match 69.1%; Score 38; DB 2; Length 1644;
Best Local Similarity 87.5%; Pred. No. 30;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 LTVAYMDY 11
|||||:
Db 1245 LTVAYMDF 1252

RESULT 3
T46408
hypothetical protein DKFZp434E1722.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C/Accession: T46408
R/Blum, H.; Bauerbach, S.; Mewes, H.W.; Gaesshuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A/Reference number: Z23034
A/Accession: T46408
A/Status: preliminary
A/Molecule type: mRNA
A/Idgenes: 1-190 <AAA>
A/References: EMBL:AL137464
Experimental source: adult testis; clone DKFZp434E1722
C/Genetics:

Query Match 67.3%; Score 37; DB 2; Length 190;
Best Local Similarity 54.5%; Pred. No. 5.4;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 RVSLTAYAMD 11
:::|||||:
Db 127 KMSLNAYALDF 137

RESULT 4
T35266
probable oxidoreductase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C/Accession: T35266
R/Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Randsdram, M.A.
submitted to the EMBL Data Library, April 1999
A/Reference number: Z21573
A/Accession: T35266
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-345 <DLI>
A/Cross-references: EMBL:AL049587; PIDN:CA840691.1; GSPDB:GN00070; SCOEDB:SCSF2A.24
Experimental source: strain A3(2)
A/Idgenes:
A/Status: SCOEDB:SCSF2A.24

Query Match 63.6%; Score 35; DB 2; Length 345;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RVSLTAYAMD 10
|||:|||:
Db 280 RVRLTAYRLD 289

RESULT 5
G96020
conserved hypothetical exported protein Smb20724 [imported] - Sinorhizobium meliloti (st
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C/Accession: G96020
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A/Reference number: A95842; MUID:21396508; PMID:1181431
A/Accession: G96020
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-314 <KUR>
A/Cross-references: GB:AL591985; PIDN:CA649831.1; PID:g15141319; GSPDB:GN00167
A/Experimental source: strain 1021, megaplasmid pSymB
R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kies, E.; Komp, C.; Lelaure,
hepault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104
A/Contents: annotation
C/Genetics:
A/Genome: Smb20724
A/Status: Smb20724

Query Match 61.8%; Score 34; DB 2; Length 314;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 VSLTAYAMD 11
:::|||||:
Db 14 IALPAYADY 23

RESULT 6
H83714
alanine racemase BH0520 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: H83714
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: H83714
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-388 <STO>
A/Cross-references: GB:AF001508; GB:BA000004; NID:g10172890; PIDN:BAB04239.1; GSPDB:GN00
A/Experimental source: strain C-125
A/Idgenes:
A/Status: BH0520
C/Superfamily: alanine racemase

Query Match 61.8%; Score 34; DB 2; Length 388;
Best Local Similarity 45.5%; Pred. No. 46;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 RVSLTAYAMD 11
||:|||||:
Db 101 RITLTVYQLDW 111

RESULT 7
S46630
hypothetical protein YJL201w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein J0325
C/Species: Saccharomyces cerevisiae
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Oct-1999
C/Accession: S46630; S30800; S56988
R/Purnelle, B.; Cosser, F.; Goffeau, A.
Yeast 10, 1235-1249, 1994
A/Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies
ase gene ACO1 and two homologues to chromosome III genes.
A/Reference number: S46621; MUID:95274326; PMID:7754713
A/Accession: S46630
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-539 <PUR>
A/Cross-references: EMBL:X77688; NID:g1183992; PIDN:CA54756.1; PID:G547591
R/Arnas, J.E.; Abelson, J.N.

submitted to the EMBL Data Library, December 1992
A:Description: The Saccharomyces cerevisiae PRP21 gene product is required for pre-splid
A:Reference number: S30799
A:Accession: S30800
A:Molecule type: DNA
A:Residues: 1-333 <ARE>
A:Cross-references: EMBL:L07744; NID:g172275; PIDN:AAB09602.1; PID:g402334
R:Purille, B.; Coster, F.; Goffeau, A.
Submitted to the Protein Sequence Database, September 1995
A:Reference number: S56977
A:Accession: S56988
A:Molecule type: DNA
A:Residues: 1-599 <PUW>
A:Cross-references: EMBL:249476; NID:g1008420; PIDN:CAA89496.1; PID:g1008421; MIPS:YUL20
C:Genetics:
A:Gene: SGD:ECM25
A:Cross-references: SGD:S0003737; MIPS:YUL201w
A:Map position: 10L

Query Match
Best Local Similarity 61.8%; Score 34; DB 2; Length 599;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVSLTRAYAMDY 11
DB 157 RLSLNVLYDY 167

RESULT 8
S14270
alcohol dehydrogenase, membrane-bound (EC 1.1.-.-) 72k chain precursor - Acetobacter pol
C:Species: Acetobacter polyoxogenes
A:Variety: strain NB11028
C:Date: 21-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
C:Accession: S14270
R:Tanaka, T.; Fukaya, M.; Takemura, H.; Tayama, K.; Okumura, H.; Kawamura, Y.; Nishiyama
Biochim. Biophys. Acta 1088, 292-300, 1991
A:Title: Cloning and sequencing of the gene cluster encoding two subunits of membrane-bc
A:Reference number: S14270; MUID:91159482; PMID:2001402
A:Accession: S14270
A:Molecule type: DNA
A:Residues: 1-738 <TAM>
A:Cross-references: GB:D00635; NID:g216185; PIDN:BAA00528.1; PID:g216186
A:Experimental source: strain NB11028
C:Complex: heterodimer of 72k and 44k chains
C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C:Keywords: alcohol metabolism; membrane protein; oxidoreductase
C:Domain: signal sequence #status predicted <Sig>
C:Product: alcohol dehydrogenase 72k chain #status predicted <MAT>

Query Match
Best Local Similarity 61.8%; Score 34; DB 2; Length 738;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTRAYAMD 10
DB 685 RGALTRAYGMD 694

RESULT 9
J50326
alcohol dehydrogenase (EC 1.1.-.-) 72k chain precursor - Acetobacter acet
C:Species: Acetobacter acet
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C:Accession: J50326
R:Inoue, T.; Sunagawa, M.; Mori, A.; Inai, C.; Fukuda, M.; Takagi, M.; Yano, K.
J. Bacteriol. 171, 3115-3122, 1989
A:Title: Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase suh
A:Reference number: J50326; MUID:89255070; PMID:2722742
A:Accession: J50326
A:Molecule type: DNA
A:Residues: 1-742 <INO>
A:Cross-references: GB:D90004; GB:M26951; NID:g216193; PIDN:BAA14058.1; PID:g216194

A:Experimental source: strain K6033
A>Note: amino terminal of mature protein is confirmed
C:Genetics:
A:Gene: adh1
C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C:Keywords: alcohol metabolism; NAD; oxidoreductase
F:1-35/Domain: signal sequence #status predicted <Sig>
F:36-742/Product: alcohol dehydrogenase 72k dehydrogenase chain #status predicted <ADC>

Query Match
Best Local Similarity 61.8%; Score 34; DB 2; Length 742;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTRAYAMD 10
DB 684 RGALTRAYGMD 693

RESULT 10
A49340
alcohol dehydrogenase (EC 1.1.-.-) precursor - Acetobacter pasteurianus (strain NC11380)
C:Species: Acetobacter pasteurianus
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Jun-2000
C:Accession: A49340
R:Takemura, H.; Kondo, K.; Horinouchi, S.; Beppu, T.
J. Bacteriol. 175, 6857-6866, 1993
A:Title: Induction by ethanol of alcohol dehydrogenase activity in Acetobacter pasteuria
A:Reference number: A49340; MUID:94042848; PMID:8226628
A:Accession: A49340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-742 <TAK>
A:Cross-references: GB:D13893; NID:g517067; PIDN:BAA40252.1; PID:g452586
C:Superfamily: glucose dehydrogenase (pyrroloquinoline-quinone)
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match
Best Local Similarity 61.8%; Score 34; DB 2; Length 742;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTRAYAMD 10
DB 684 RGALTRAYGMD 693

RESULT 11
B91052
hypothetical protein ECs3386 [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: B91052
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gesawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156531; PMID:11258796
A:Accession: B91052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1653 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA836809.1; PID:g13362856; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs3386

Query Match
Best Local Similarity 61.8%; Score 34; DB 2; Length 1653;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTRAYAMDY 11
DB 1253 LTRAYVMDR 1260

RESULT 12

P85896

hypothetical protein 23787 [imported] - Escherichia coli (strain O157:H7, substrain EDL5

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: F85896

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousta, K.; Apodaca,

Nature 409 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F85896

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1653 <GTO>

A:Cross-references: GB:AE005174; NID:g12516921; PIDN:AAG57634.1; GSPDB:GN00145; UMGF:237

C:Genetics: C:Experimental source: strain O157:H7, substrain EDL933

C:Gene: 23787

Query Match

Best Local Similarity

Matches

6; Conservative

1; Mismatches

1; Indels

0; Gaps

0;

Db

1253 LTAYVMDP 1260

QY

4 LTAYVMDY 11

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C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity

Matches

6; Conservative

2; Mismatches

1; Indels

0; Gaps

0;

Db

28 SLTAYGVDM 36

QY

3 SLTAYVMDY 11

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RESULT 15

B53285

Ig heavy chain V and J regions, monoclonal antibody OHP101.B11.1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: B53285

R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

Mol. Immunol. 28, 1063-1072, 1991

A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struc

and their pH-reactivity profiles.

A:Reference number: A53285; MUID:92017897; PMID:1922102

A:Accession: B53285

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-119 <SAM>

A:Note: sequence inconsistent with nucleotide translation

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity

Matches

7; Conservative

0; Mismatches

4; Indels

0; Gaps

0;

Db

98 RGLRRYVMDY 108

QY

1 RVSLLTAYVMDY 11

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Search completed: September 10, 2003, 17:42:42

Job time: 16.85 secs

RESULT 14

S32786

Ig heavy chain (anti-biotin) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S32786

R:Bagci, H.; Kohen, F.; Kuscuglu, U.; Bayer, E.A.; Wiltchek, M.

FEBS Lett. 322, 47-50, 1993

A:Title: Monoclonal anti-biotin antibodies simulate avidin in the recognition of biotin.

A:Reference number: S32786; MUID:93245957; PMID:8482366

A:Accession: S32786

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-118 <BAG>

A:Cross-references: GB:S59639; NID:g299965; PIDN:AAB26438.1; PID:g299966

C:Superfamily: immunoglobulin V region; immunoglobulin homology

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:42:07 ; Search time 22 Seconds
(without alignments)
72.956 Million cell updates/sec

Title: US-09-759-112A-19
Perfect score: 55
Sequence: 1 RVSLLAYAMDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	11	11	US-09-759-112A-19
2	55	100.0	121	11	US-09-759-112A-7
3	55	63.6	329	15	US-10-156-761-9210
4	34	61.8	130	9	US-09-802-077-5
5	34	61.8	130	9	US-09-802-096-5
6	34	61.8	130	11	US-09-925-179-5
7	34	61.8	249	9	US-09-730-374-3
8	34	61.8	1046	15	US-10-128-714-3288
9	34	61.8	1199	15	US-10-128-714-8288
10	34	61.8	1653	9	US-09-741-669-402
11	33	60.0	16	11	US-09-880-748-2309
12	33	60.0	130	9	US-09-925-299-999
13	33	60.0	130	11	US-09-925-299-999
14	33	60.0	251	11	US-09-880-748-231
15	33	60.0	329	12	US-10-238-075-368

16	33	60.0	604	12	US-10-303-664A-57	Sequence 57, Appl
17	33	60.0	687	12	US-10-181-319-2	Sequence 2, Appl
18	33	60.0	1010	12	US-10-238-075-945	Sequence 945, Ap
19	32	58.2	16	11	US-09-880-748-2253	Sequence 2253, Ap
20	32	58.2	147	9	US-09-797-481-4	Sequence 4, Appl
21	32	58.2	147	9	US-09-844-736-6	Sequence 6, Appl
22	32	58.2	147	15	US-10-162-396-6	Sequence 1043, A
23	32	58.2	181	15	US-10-156-761-10043	Sequence 237, Ap
24	32	58.2	251	11	US-09-880-748-237	Sequence 12, Appl
25	32	58.2	264	15	US-10-167-015-12	Sequence 4, Appl
26	32	58.2	326	9	US-09-943-002-4	Sequence 11450, A
27	32	58.2	409	15	US-10-156-761-11450	Sequence 10462, A
28	32	58.2	602	15	US-10-156-761-10462	Sequence 2, Appl
29	32	58.2	677	15	US-10-284-668-2	Sequence 33, Appl
30	32	58.2	986	10	US-09-870-759-33	Sequence 13, Appl
31	32	58.2	986	12	US-09-751-108A-33	Sequence 2244, Ap
32	32	58.2	1197	15	US-10-284-668-12	Sequence 1137, Ap
33	31	56.4	16	11	US-09-880-748-2244	Sequence 4633, Ap
34	31	56.4	66	11	US-09-764-891-4633	Sequence 1137, Ap
35	31	56.4	196	10	US-09-764-864-1137	Sequence 92, Appl
36	31	56.4	251	11	US-09-880-748-92	Sequence 21, Appl
37	31	56.4	268	11	US-09-557-796-21	Sequence 20, Appl
38	31	56.4	303	10	US-09-866-572A-20	Sequence 2, Appl
39	31	56.4	303	10	US-09-866-570A-20	Sequence 20, Appl
40	31	56.4	303	15	US-10-166-984-20	Sequence 5, Appl
41	31	56.4	340	9	US-09-775-195-2	Sequence 6, Appl
42	31	56.4	340	9	US-09-775-195-5	Sequence 2, Appl
43	31	56.4	340	9	US-09-775-195-6	Sequence 6, Appl
44	31	56.4	340	15	US-10-155-947-2	Sequence 2, Appl
45	31	56.4	340	15	US-10-155-947-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-759-112A-19
; Sequence 19, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1P7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1P7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759, 112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: mouse
US-09-759-112A-19

Query Match 100.0%; Score 55; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVSLLAYAMDY 11
DB 1 RVSLLAYAMDY 11

RESULT 2
US-09-759-112A-7
; Sequence 7, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT

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; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mouse
US-09-759-112A-7

Query Match          100.0%; Score 55; DB 11; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVSLTAYAMDY 11
        |||||
        100 RVSLTAYAMDY 110

RESULT 3
US-10-156-761-9210
; Sequence 9210, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHYUKA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9210
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Streptomyces avermectilis
US-10-156-761-9210

Query Match          63.6%; Score 35; DB 15; Length 339;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RVSLTAYAMD 10
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        280 RVRLTAYRLD 289

RESULT 4
US-09-802-077-5
; Sequence 5, Application US/09802077
; Patent No. US2001003342A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
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; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-5

Query Match          61.8%; Score 34; DB 9; Length 130;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 LTRAYAMDY 11
        :|||
        99 VVAYAMDY 106

RESULT 5
US-09-802-096-5
; Sequence 5, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-5

Query Match          61.8%; Score 34; DB 9; Length 130;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 LTRAYAMDY 11
        :|||
        99 VVAYAMDY 106

RESULT 6
US-09-925-179-5
; Sequence 5, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-19E Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
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;; PRIOR FILING DATE: 1995-03-15
;; PRIOR APPLICATION NUMBER: US 08/185,899
;; PRIOR FILING DATE: 1994-01-26
;; PRIOR APPLICATION NUMBER: PCT/US92/06860
;; PRIOR FILING DATE: 1992-08-14
;; PRIOR APPLICATION NUMBER: US 07/879,495
;; PRIOR FILING DATE: 1992-05-07
;; PRIOR APPLICATION NUMBER: US 07/744,768
;; PRIOR FILING DATE: 1991-08-14
;; NUMBER OF SEQ ID NOS: 68
;; SEQ ID NO 5
;; LENGTH: 130
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-925-179-5

Query Match
Best Local Similarity 61.8%; Score 34; DB 11; Length 130;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

4 LTAYAMDY 11
:|||||
99 VVAYAMDY 106

RESULT 7
US-09-730-374-3
;; Sequence 3, Application US/09730374
;; Patent No. US20010031261A1
;; GENERAL INFORMATION:
;; APPLICANT: Lust, John A.
;; APPLICANT: Donovan, Kathleen A.
;; TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES
;; TITLE OF INVENTION: TO CD38 TO TREAT MULTIPLE MYELOMA
;; FILE REFERENCE: 150.188US2
;; CURRENT FILING DATE: 2001-05-10
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: PCT/US99/12512
;; PRIOR FILING DATE: 1999-06-04
;; PRIOR APPLICATION NUMBER: 60/088,277
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: A polypeptide encoded by an open reading frame of
;; OTHER INFORMATION: SEQ ID NO:1
US-09-730-374-3

Query Match
Best Local Similarity 61.8%; Score 34; DB 9; Length 249;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TAYAMDY 11
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DB 108 TGYAMDY 114

RESULT 8
US-10-128-714-3288
;; Sequence 3288, Application US/10128714
;; Publication No. US20030119013A1
;; GENERAL INFORMATION:
;; APPLICANT: Jiang, Bo
;; APPLICANT: Hu, Weng
;; APPLICANT: Tishkoff, Daniel
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Eroshkin, Alexey M
;; APPLICANT: Lemieux, Sebastien M
;; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

;; TITLE OF INVENTION: Methods of Use
;; FILE REFERENCE: 10182-018-999
;; CURRENT APPLICATION NUMBER: US/10/128,714
;; CURRENT FILING DATE: 2002-04-23
;; PRIOR APPLICATION NUMBER: US 60/285,697
;; PRIOR FILING DATE: 2001-04-23
;; PRIOR APPLICATION NUMBER: US 60/287,066
;; PRIOR FILING DATE: 2001-04-27
;; PRIOR APPLICATION NUMBER: US 60/295,890
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: US 60/303,899
;; PRIOR FILING DATE: 2001-07-09
;; PRIOR APPLICATION NUMBER: US 60/316,362
;; PRIOR FILING DATE: 2001-08-31
;; NUMBER OF SEQ ID NOS: 8603
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 3288
;; LENGTH: 1046
;; TYPE: PRT
;; ORGANISM: Aspergillus fumigatus
US-10-128-714-3288

Query Match
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Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSLTAYAMD 10
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DB 69 MSLTSYSMD 77

RESULT 9
US-10-128-714-8288
;; Sequence 8288, Application US/10128714
;; Publication No. US20030119013A1
;; GENERAL INFORMATION:
;; APPLICANT: Jiang, Bo
;; APPLICANT: Hu, Weng
;; APPLICANT: Tishkoff, Daniel
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Eroshkin, Alexey M
;; APPLICANT: Lemieux, Sebastien M
;; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
;; FILE REFERENCE: 10182-018-999
;; CURRENT APPLICATION NUMBER: US/10/128,714
;; CURRENT FILING DATE: 2002-04-23
;; PRIOR APPLICATION NUMBER: US 60/285,697
;; PRIOR FILING DATE: 2001-04-23
;; PRIOR APPLICATION NUMBER: US 60/287,066
;; PRIOR FILING DATE: 2001-04-27
;; PRIOR APPLICATION NUMBER: US 60/295,890
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: US 60/303,899
;; PRIOR FILING DATE: 2001-07-09
;; PRIOR APPLICATION NUMBER: US 60/316,362
;; PRIOR FILING DATE: 2001-08-31
;; NUMBER OF SEQ ID NOS: 8603
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 8288
;; LENGTH: 1199
;; TYPE: PRT
;; ORGANISM: Aspergillus fumigatus
US-10-128-714-8288

Query Match
Best Local Similarity 61.8%; Score 34; DB 15; Length 1199;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSLTAYAMD 10
:|||||
DB 212 MSLTSYSMD 220

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Best Local Similarity      55.6%;      Fred. No. 5.3;
Matches      5; Conservative      3; Mismatches      1; Indels      0; Gaps      0
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Db      5 TLTSYVLDY 13

RESULT 12
US-09-925-289-999
: Sequence 999, Application US/099252299

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Best Local Similarity 60.0%; Pred. No. 50;
Matches      6; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

QY      2 VSLTAYAMDY 11
      : | | | | |
      : | | | | |
Db      88 MKLLAYAMDF 97

RESULT 14
US-09-880-748-231
; Sequence 231, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 231
 ; LENGTH: 251
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-231

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 Best Local Similarity 55.6%; Pred. No. 1e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

3 SLTAYAMDY 11
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 103 TLTSYVLDY 111

RESULT 15
 US-10-238-075-368
 ; Sequence 368, Application US/10238075
 ; Publication No. US20030148324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: I.N.S.E.R.M.
 ; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
 ; FILE REFERENCE: BLANDINE
 ; CURRENT APPLICATION NUMBER: US/10/238,075
 ; PRIOR FILING DATE: 2002-09-10
 ; PRIOR APPLICATION NUMBER: 0003145
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 1576
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 368
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-10-238-075-368

Query Match 60.0%; Score 33; DB 12; Length 329;
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 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 2 VSLTAYAMDY 11
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OM protein - protein search, using sw model

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Title: US-09-759-112A-19
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	39	3	US-08-984-277-10
2	42	76.4	120	2	US-08-652-558-4
3	42	76.4	120	2	US-08-652-558-5
4	42	76.4	120	2	US-08-652-558-6
5	42	76.4	120	2	US-08-652-558-7
6	42	76.4	120	2	US-08-652-558-8
7	42	76.4	120	2	US-08-652-558-9
8	42	76.4	120	2	US-08-652-558-38
9	42	76.4	120	3	US-09-254-189-2
10	42	76.4	120	3	US-09-254-189-3
11	42	76.4	120	3	US-09-254-189-4
12	42	76.4	120	3	US-09-254-189-5
13	42	76.4	120	3	US-09-254-189-6
14	34	61.8	130	4	US-08-466-151-5
15	34	61.8	130	4	US-08-466-151-6
16	34	61.8	138	3	US-08-513-968-4
17	34	61.8	138	3	US-09-070-637-20
18	34	61.8	738	1	US-07-985-458-3
19	33	60.0	452	1	US-08-275-488A-2
20	33	60.0	452	1	US-08-275-490-2
21	33	60.0	452	1	US-08-446-380-2
22	33	60.0	452	1	US-08-446-374-2
23	33	60.0	452	1	US-08-445-382-2
24	33	60.0	452	1	US-08-445-801-2
25	33	60.0	452	1	US-08-275-487-2
26	33	60.0	452	5	PCT-US95-08919-2
27	33	60.0	453	1	US-08-275-488A-12

28	33	60.0	453	1	US-08-275-490-12	Sequence 12, Appl
29	33	60.0	453	1	US-08-446-380-12	Sequence 12, Appl
30	33	60.0	453	1	US-08-446-374-12	Sequence 12, Appl
31	33	60.0	453	1	US-08-446-382-12	Sequence 12, Appl
32	33	60.0	453	1	US-08-445-801-12	Sequence 12, Appl
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41	33	60.0	494	1	US-08-275-487-4	Sequence 4, Appl
42	33	60.0	494	5	PCT-US95-08919-4	Sequence 4, Appl
43	33	60.0	601	4	US-09-252-991A-30589	Sequence 30589, A
44	32	58.2	130	4	US-09-252-991A-23553	Sequence 23553, A
45	32	58.2	147	2	US-08-579-940-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-984-277-10
; Sequence 10, Application US/08984277
; Patent No. 6057421
; GENERAL INFORMATION:
; APPLICANT: Muller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1F7
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,277
; FILING DATE: 3-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca, Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50200-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; TELEEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-984-277-10
Query Match 100.0%; Score 55; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. NO. 0.00015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RVSLTAYAMDY 11

Db 18 RVSLTAVAMDY 28

RESULT 2

US-08-652-558-4
Sequence 4, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-4

ry Match 76.4%; Score 42; DB 2; Length 120;
c Local Similarity 72.7%; Pred. No. 0.25;
ches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAVAMDY 11
Db 99 RVATATLYAMDY 109

RESULT 3

US-08-652-558-5
Sequence 5, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-5

Query Match 76.4%; Score 42; DB 2; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLTAVAMDY 11
Db 99 RVATATLYAMDY 109

RESULT 4

US-08-652-558-6
Sequence 6, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-6

Query Match 76.4%; Score 42; DB 2; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSATVAMDY 11
||:|||||
Db 99 RVTATLYAMDY 109

RESULT 5
US-08-652-558-7
Sequence 7, Application US/08652558
Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
THEREOF

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9100

TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-558-7

Query Match 76.4%; Score 42; DB 2; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSATVAMDY 11
||:|||||
Db 99 RVTATLYAMDY 109

RESULT 6
US-08-652-558-8
Sequence 8, Application US/08652558
Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9111

TELEFAX: 617-345-9100

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-558-8

Query Match 76.4%; Score 42; DB 2; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSATVAMDY 11
||:|||||
Db 99 RVTATLYAMDY 109

RESULT 7
US-08-652-558-9
Sequence 9, Application US/08652558
Patent No. 5861155

GENERAL INFORMATION:

APPLICANT: LIN, AUGUSTINE YEE-THARN

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,558

FILING DATE: JUNE 6, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB94/00387

FILING DATE: NOVEMBER 21, 1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-9

Query Match 76.4%; Score 42; DB 2; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 RVSLEYAMDY 11
||: |||||
99 RVTATLYAMDY 109

RESULT 8
US-08-652-558-38
Sequence 38, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-THARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCORP
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-38

Query Match 76.4%; Score 42; DB 2; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RVSLEYAMDY 11
||: |||||

Db 99 RVTATLYAMDY 109

RESULT 9
US-09-254-189-2
Sequence 2, Application US/09254189
Patent No. 6150792
GENERAL INFORMATION:
APPLICANT: Lundquist, Tomas
TITLE OF INVENTION: Sequence Listing
Patent No. 6150792
FILE REFERENCE: 3526/00000
CURRENT APPLICATION NUMBER: US/09/254,189
CURRENT FILING DATE: 1999-03-02
EARLIER APPLICATION NUMBER: 00/000,000
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:humanized
US-09-254-189-2

Query Match 76.4%; Score 42; DB 3; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLEYAMDY 11
||: |||||
Db 99 RVTATLYAMDY 109

RESULT 10
US-09-254-189-3
Sequence 3, Application US/09254189
Patent No. 6150792
GENERAL INFORMATION:
APPLICANT: Lundquist, Tomas
TITLE OF INVENTION: Sequence Listing
Patent No. 6150792
FILE REFERENCE: 3526/00000
CURRENT APPLICATION NUMBER: US/09/254,189
CURRENT FILING DATE: 1999-03-02
EARLIER APPLICATION NUMBER: 00/000,000
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:humanized
US-09-254-189-3

Query Match 76.4%; Score 42; DB 3; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLEYAMDY 11
||: |||||
Db 99 RVTATLYAMDY 109

RESULT 11
US-09-254-189-4
Sequence 4, Application US/09254189
Patent No. 6150792

```
;; GENERAL INFORMATION:
;; APPLICANT: Lundquist, Tomas
;; TITLE OF INVENTION: Sequence Listing
;; Patent No. 6150792
;; FILE REFERENCE: 3526/00000
;; CURRENT APPLICATION NUMBER: US/09/254,189
;; CURRENT FILING DATE: 1999-03-02
;; EARLIER APPLICATION NUMBER: 00/000,000
;; EARLIER FILING DATE: 1998-11-24
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 120
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:humanized
;; OTHER INFORMATION: monoclonal antibody
;; US-09-254-189-4

Query Match      76.4%; Score 42; DB 3; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches      8; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Qy      1 RVSLTAYAMDY 11
Db      99 RVTATLYAMDY 109

RESULT 12
US-09-254-189-5
; Sequence 5, Application US/09254189
; Patent No. 6150792
; GENERAL INFORMATION:
; APPLICANT: Lundquist, Tomas
; TITLE OF INVENTION: Sequence Listing
; Patent No. 6150792
; FILE REFERENCE: 3526/00000
; CURRENT APPLICATION NUMBER: US/09/254,189
; CURRENT FILING DATE: 1999-03-02
; EARLIER APPLICATION NUMBER: 00/000,000
; EARLIER FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; OTHER INFORMATION: monoclonal antibody
;; US-09-254-189-5

Query Match      76.4%; Score 42; DB 3; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches      8; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Qy      1 RVSLTAYAMDY 11
Db      99 RVTATLYAMDY 109

RESULT 13
US-09-254-189-6
; Sequence 6, Application US/09254189
; Patent No. 6150792
; GENERAL INFORMATION:
; APPLICANT: Lundquist, Tomas
; TITLE OF INVENTION: Sequence Listing
; Patent No. 6150792
; FILE REFERENCE: 3526/00000
; CURRENT APPLICATION NUMBER: US/09/254,189
; CURRENT FILING DATE: 1999-03-02
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;; EARLIER APPLICATION NUMBER: 00/000,000
;; EARLIER FILING DATE: 1998-11-24
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 120
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:humanized
;; OTHER INFORMATION: monoclonal antibody
;; US-09-254-189-6

Query Match      76.4%; Score 42; DB 3; Length 120;
Best Local Similarity 72.7%; Pred. No. 0.25;
Matches      8; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Qy      1 RVSLTAYAMDY 11
Db      99 RVTATLYAMDY 109

RESULT 14
US-08-466-151-5
; Sequence 5, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/225-1489
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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US-08-466-151-5

Query Match 61.8%; Score 34; DB 3; Length 130;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTRAYAMDY 11
: |||||
Db 99 VVAYAMDY 106

RESULT 15

US-08-466-163B-5
; Sequence 5, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2CID1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 5
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-5

Query Match 61.8%; Score 34; DB 4; Length 130;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTRAYAMDY 11
: |||||
Db 99 VVAYAMDY 106

Search completed: September 10, 2003, 17:43:22
Web time : 15.95 secs

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OM protein - protein search, using sw model

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(without alignments)
44.712 Million cell updates/sec

Title: US-09-759-112a-19
Perfect score: 55
Sequence: 1 RVSLTAYAMDY 11

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Post-processing: Minimum Match 0%
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	55	100.0	11	23	AAO18534	Murine Mab 1F7 hea
2	55	100.0	39	21	AAV91019	1F7 antibody varia
3	55	100.0	121	23	AAO18528	Murine Mab 1F7 hea
4	42	76.4	120	20	AAV22433	TM27 antibody VH c
5	42	76.4	120	20	AAV22429	TM27 antibody VH c
6	42	76.4	120	20	AAV22430	TM27 antibody VH c
7	42	76.4	120	20	AAV22431	TM27 antibody VH c
8	42	76.4	120	20	AAV22432	TM27 antibody VH c
9	37	67.3	378	22	ABG09046	Novel human diagno

10	37	67.3	391	23	ABP43853
11	37	67.3	1712	24	AAO16433
12	35	63.6	120	16	AAV77303
13	35	63.6	424	21	AAV91067
14	34	61.8	119	10	AAV90540
15	34	61.8	119	13	AAV24555
16	34	61.8	119	13	AAV24556
17	34	61.8	119	13	AAV24557
18	34	61.8	119	13	AAV24558
19	34	61.8	119	13	AAV24560
20	34	61.8	119	13	AAV24561
21	34	61.8	119	13	AAV24562
22	34	61.8	130	14	AAV33308
23	34	61.8	130	21	AAV85196
24	34	61.8	138	10	AAV90542
25	34	61.8	143	21	AAV43867
26	34	61.8	249	21	AAV69523
27	34	61.8	370	22	AAV94366
28	34	61.8	370	23	AAE21711
29	34	61.8	370	24	AAO16375
30	34	61.8	370	24	AAO16379
31	34	61.8	633	20	AAV87786
32	34	61.8	738	12	AAV13993
33	34	61.8	738	13	AAV20192
34	34	61.8	742	11	AAV05235
35	34	61.8	1046	24	ABJ25630
36	34	61.8	1199	24	ABJ26230
37	34	61.8	1653	22	AAV98354
38	33.5	60.9	247	9	AAV80155
39	33.5	60.9	247	9	AAV80156
40	33.5	60.9	466	5	AAV40032
41	33	60.0	16	23	ABP46298
42	33	60.0	61	21	AAV21232
43	33	60.0	80	21	AAV21231
44	33	60.0	91	21	AAV54795
45	33	60.0	106	21	AAV21230

ALIGNMENTS

RESULT 1
ID AAO18534 strand: Peptide: 11 AA.
AC AAO18534;
XX
DT 11-OCT-2002 (first entry)
XX
DE Murine Mab 1F7 heavy chain CDR3 region.
XX
KW Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
KW Complementarity determining region; framework-determining region;
KW FR; heavy chain; light chain; HIV infection.
XX
OS Mus sp.
XX
PN WO20025566-A2.
XX
PD 18-JUL-2002.
XX
PF 11-JAN-2002; 2002WO-US00927.
XX
PR 11-JAN-2001; 2001US-0759112.
XX
PA (IMMP-) IMMOPHERON INC.
XX
PI Muller S, Kohler H;
XX
DR WPI: 2002-590668/63.
DR N-PSDB; AAL48658.
XX
PT New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate
PT anti- human immunodeficiency virus (HIV) antibodies, for use in
PT vaccines against HIV -

PS Claim 4, Page 22, 27pp; English.

CC The present invention relates to coding sequences of the murine 1F7
CC anti-idiotypic antibody complementarity-determining region (CDR) or
CC framework-determining region (FR). The antibody binds to human or primate
CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the
CC treatment of HIV infection. The present sequence is a region of the 1F7
CC heavy chain.

XX Sequence 11 AA;

Query Match 100.0%; Score 55; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;

1 RVSLETAAYMDY 11
|||||||
1 RVSLETAAYMDY 11

RESULT 2

AAV91019 standard; protein; 39 AA.

AAV91019;

05-SEP-2000 (first entry)

1F7 antibody variable heavy chain H3 amino acid sequence SEQ ID NO:10.

1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
AIDS; anti-HIV; human immunodeficiency virus; detection;

acquired immunodeficiency syndrome.

Mus sp.

US6057421-A.

02-MAY-2000.

03-DEC-1997; 97US-0984277.

30-NOV-1994; 94US-0351193.

(IMMP-) IMPHERON INC.

Muller S, Kohler H;

WPI; 2000-338622/29.

Variable heavy and light chain regions of murine monoclonal antibody

1F7, useful for treating HIV infection and AIDS -

Claim 1; Fig 8; 45pp; English.

CC The present invention describes the variable heavy and light chain
CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAV91014 to
CC AAV91016 represent specifically claimed amino acid sequences of the
CC variable light chain, and AAV91017 to AAV91019 represent specifically
CC claimed amino acid sequence of the variable heavy chain. The antibodies
CC are used for treatment of HIV (human immunodeficiency virus) infection
CC and AIDS (acquired immunodeficiency syndrome). They are also used for
CC detecting HIV in serum and for stimulating HIV antigen related and
CC committed B cells to produce broadly reactive and neutralising antibodies
CC by clonotypic stimulation.

Sequence 39 AA;

Query; Match 100.0%; Score 55; DB 21; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVSLETAAYMDY 11
|||||||
Db 18 RVSLETAAYMDY 28

RESULT 3

AA018528 standard; Protein; 121 AA.

AA018528;

11-OCT-2002 (first entry)

Murine Mab 1F7 heavy chain.

Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;

complementarity determining region; framework-determining region;

FR; heavy chain; light chain; HIV infection.

Mus sp.

WO200255668-A2.

11-JAN-2002; 2002WO-US00927.

11-JAN-2001; 2001US-0759112.

(IMMP-) IMPHERON INC.

Muller S, Kohler H;

WPI; 2002-590668/63.

N-PSDB; AAL48652.

PT New polynucleotide encoding a complementarity- or framework-determining
PT region of an anti-idiotypic antibody that binds to human or primate
PT anti- human immunodeficiency virus (HIV) antibodies, for use in
PT vaccines against HIV -

PS Disclosure; Page 18-19; 27pp; English.

CC The present invention relates to coding sequences of the murine 1F7

CC anti-idiotypic antibody complementarity-determining region (CDR) or

CC framework-determining region (FR). The antibody binds to human or primate

CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the

CC treatment of HIV infection. The present sequence is the 1F7 heavy chain.

Sequence 121 AA;

QY 1 RVSLETAAYMDY 11
|||||||
Db 100 RVSLETAAYMDY 110

RESULT 4

AAV22433 standard; protein; 120 AA.

AAV22433;

28-SEP-1999 (first entry)

TM27 antibody VH chain mutant V92R.

Sequence 120 AA;

Query; Match 100.0%; Score 55; DB 21; Length 39;

```

KW Igg antibody; TM27; variable chain; immunoglobulin G; medical therapy;
KV autoimmune disease; multiple sclerosis; antibody storage; VH; mutuin;
KM heavy chain.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 92
FT /label= V92R
PI
XX
XX WO9337329-A1.
PN
XX
XX 29-JUL-1999.
PD
XX
XX 15-JAN-1999; 99WO-SE00049.
PF
XX 09-MAR-1998; 98SE-0000766.
PR
XX 22-JAN-1998; 98SE-0000170.
XX
XX (ASTR ) ASTRA AB.
XX
XX Flank O, Petren S;
DR WPI; 1999-458611/38.
XX
XX Isotonic pharmaceutical antibody formulations comprising a citrate
PT buffer, have improved storage
XX
XX Claim 12; Page 25-26; 30pp; English.
XX
XX This sequence is a mutant of the variable heavy (VH) chain of the
CC antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in
CC the isotonic pharmaceutical formulation of the invention, along with a
CC citrate buffer at a physiologically acceptable pH. The formulations are
CC useful in medical therapy, especially for treatment of autoimmune
CC disease, and particularly, therapy of multiple sclerosis (using the TM27
CC antibody heavy or light chains). The formulation is useful for improving
CC the storage of an antibody. The antibody formulations are simple and
CC effective. The formulations are stable and have improved storage
CC properties. The formulation is simpler than prior art formulations.
CC Existing antibody formulations require the use both of a stabiliser and a
CC buffer. The present invention formulations are stabilized only by citrate
CC buffer in a saline solution at a physiologically preferable pH. The
CC avoidance of low pH prevents undesirable reaction as the site of
CC infection. The formulation does not use ovalbumin for stabilisation,
CC hence avoiding an allergic response to ovalbumin. Also the formulation
CC does not require lyophilisation which is an expensive process and also
CC requires the formulation to be resuspended prior to administration.
XX
XX Sequence 120 AA:
XX
XX Query Match 76.4%; Score 42; DB 20; Length 120;
XX Best Local Similarity 72.7%; Pred. No. 0.8;
XX Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0
XX
XX 1 RVSLTAYAMDY 11
XX ||:|||||
XX 99 RVTATLYAMDY 109
XX
XX RESULT 5
XX ID AAY22429 standard; protein; 120 AA.
XX AC AAY22429;
XX
XX 28-SEP-1999 (first entry)
XX
XX TM27 antibody VH chain.
XX
XX IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy;
KM autoimmune disease; multiple sclerosis; antibody storage; VH;
KM heavy chain.

```

OS	Homo sapiens.
XX OS	WO9937329-A1.
XX PN	29-JUL-1999.
XX PD	15-JAN-1999; 99MO-SE00049.
PF PR	09-MAR-1998; 98SE-0000766.
PR XX	22-JAN-1998; 98SE-0000170.
PA	(ASTR) ASTRA AB.
PI Flink O,	Petren S;
DR WPI; 1999-	458611/38.
PT Isosonic pharmaceutical antibody formulations comprising a citrate buffer, have improved storage	
PS Claim 12; Page 11; 30pp; English.	
CC This sequence represents the variable heavy (VH) chain of the antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in the isotonic pharmaceutical formulation of the invention, along with a citrate buffer at a physiologically acceptable pH. The formulations are useful in medical therapy, especially for treatment of autoimmune disease, and particularly, therapy of multiple sclerosis (using the TM27 antibody heavy or light chains). The formulation is useful for improving the storage of an antibody. The antibody formulations are simple and effective. The formulations are stable and have improved storage properties. The formulation is simpler than prior art formulations. Existing antibody formulations require the use both of a stabiliser and a buffer. The present invention formulations are stabilized only by citrate buffer in a saline solution at a physiologically preferable pH. The avoidance of low pH prevents undesirable reaction as the site of infection. The formulation does not use ovalbumin for stabilisation, hence avoiding an allergic response to ovalbumin. Also the formulation does not require lyophilisation which is an expensive process and also requires the formulation to be resuspended prior to administration.	
SQ Sequence 120 AA:	
Query Match	76.4%; Score 42; DB 20; Length 120;
Best Local Similarity	72.7%; Pred. No. 0.8;
Matches	8; Conservative 1; Mismatches 2; Indels 0; Gaps 0
OY	1 RVSLSFATVMNDY 11 :: Db 99 RVTAFLTYMNDY 109
RESULT 6	
ID AAY22430	AAY22430 standard; protein; 120 AA.
AC AAY22430;	
DT DT	28-SEP-1999 (first entry)
DE XX	TM27 antibody VH chain mutant L48I.
DZ XX	IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy;
KW autoimmune disease; multiple sclerosis; antibody storage; VH, mutain;	
KX heavy chain.	
OS Homo sapiens.	
FH Key	Location/Qualifiers
FT Misc-difference 48	
XX /label= L48I	

PN MO9937329-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 15-JAN-1999; 99WO-SE00049.
 XX
 PR 09-MAR-1998; 98SE-0000766.
 XX
 PR 22-JAN-1998; 98SE-0000170.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Flink O, Petren S;
 XX
 PI WPI; 1999-458611/38.
 DR
 XX
 PT Isotonic pharmaceutical antibody formulations comprising a citrate
 PT buffer, have improved storage
 XX
 PS Claim 12; Page 20-21; 30pp; English.

This sequence is a mutant of the variable heavy (VH) chain of the antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in the isotonic pharmaceutical formulation of the invention, along with a citrate buffer at a physiologically acceptable pH. The formulations are useful in medical therapy, especially for treatment of autoimmune disease, and particularly, therapy of multiple sclerosis (using the TM27 antibody heavy or light chains). The formulation is useful for improving the storage of an antibody. The antibody formulations are simple and effective. The formulations are stable and have improved storage. Existing antibody formulations require the use both of a stabiliser and a buffer. The present invention formulations are stabilized only by citrate buffer in a saline solution at a physiologically preferable pH. The avoidance of low pH prevents undesirable reaction as the site of injection. The formulation does not use ovalbumin for stabilisation, hence avoiding an allergic response to ovalbumin. Also the formulation does not require lyophilisation which is an expensive process and also requires the formulation to be resuspended prior to administration.

SO Sequence 120 AA;
 Query Match 76.4%; Score 42; DB 20; Length 120;
 Best Local Similarity 72.7%; Pred. No. 0.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RVSLTAYAMDY 11
 ||: |||||
 99 RVTATLYAMDY 109

RESULT 7
 ID AAY22431 standard; protein; 120 AA.
 XX
 AC AAY22431;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE TM27 antibody VH chain mutant F78V, S79F.
 XX
 KM IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy;
 KM autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;
 KM heavy chain.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 78 /label= F78V
 FT Misc-difference 79 /label= S79F
 FT
 FT
 PN MO9937329-A1.

XX
 PD 29-JUL-1999.
 XX
 PF 15-JAN-1999; 99WO-SE00049.
 XX
 PR 09-MAR-1998; 98SE-0000766.
 XX
 PR 22-JAN-1998; 98SE-0000170.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Flink O, Petren S;
 XX
 PI WPI; 1999-458611/38.
 DR
 XX
 PT Isotonic pharmaceutical antibody formulations comprising a citrate
 PT buffer, have improved storage
 XX
 PS Claim 12; Page 22-23; 30pp; English.

This sequence is a mutant of the variable heavy (VH) chain of the antibody TM27. TM27 is an immunoglobulin G (IgG) antibody, contained in the isotonic pharmaceutical formulation of the invention, along with a citrate buffer at a physiologically acceptable pH. The formulations are useful in medical therapy, especially for treatment of autoimmune disease, and particularly, therapy of multiple sclerosis (using the TM27 antibody heavy or light chains). The formulation is useful for improving the storage of an antibody. The antibody formulations are simple and effective. The formulations are stable and have improved storage. Existing antibody formulations require the use both of a stabiliser and a buffer. The present invention formulations are stabilized only by citrate buffer in a saline solution at a physiologically preferable pH. The avoidance of low pH prevents undesirable reaction as the site of injection. The formulation does not use ovalbumin for stabilisation, hence avoiding an allergic response to ovalbumin. Also the formulation does not require lyophilisation which is an expensive process and also requires the formulation to be resuspended prior to administration.

SO Sequence 120 AA;
 Query Match 76.4%; Score 42; DB 20; Length 120;
 Best Local Similarity 72.7%; Pred. No. 0.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RVSLTAYAMDY 11
 ||: |||||
 99 RVTATLYAMDY 109

RESULT 8
 ID AAY22432 standard; protein; 120 AA.
 XX
 AC AAY22432;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE TM27 antibody VH chain mutant V67L, T68S, M69I, L70S, T73N.
 XX
 KM IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy;
 KM autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;
 KM heavy chain.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 67 /label= V67L
 FT Misc-difference 68 /label= T68S
 FT Misc-difference 69 /label= M69I
 FT
 FT
 FT Misc-difference 70

XX WO9516038-A2.
XX
XX 15-JUN-1995.
PD
XX
XX 21-NOV-1994; 94WO-1B00387.
XX
XX 08-DEC-1993; 93GB-0025182.
PR
XX
XX (MERC/) MERCER C P.
PA (TCEB-) T CELL SCT INC.
XX
XX Lin AY;
PI
XX WPI; 1995-224322/29.
DR
XX
XX Humanised antibody specific for select sub-population of T cells
PT useful for treatment of Crohn's disease and Multiple Sclerosis

Claim 3; Page 81; 92pp; English.

CC A mouse monoclonal antibody (mAb), TM23, which recognises human V
CC beta 5.2 and 5.3, was humanised by CDR grafting into NEMM heavy
CC chain and REI light chain frameworks. The CDNA's encoding humanised
CC heavy (IgG1) and light (K) chains in mammalian cell expression
CC vectors with Neo and DHFR selection markers, respectively, were
CC transfected into a DHFR- Chinese hamster fibroblast (CHO) cell line
CC followed by selection and amplification. The humanised mAb that was
CC secreted was designated "TM27", and maintains specificity for human
CC TCR V beta 5.2 and 5.2. It is used as a therapeutic agent for human
CC multiple sclerosis. TM27 is a mutant with Leu at posn. 48 of heavy
CC chain.
CC
CC (updated on 25-MAR-2003 to correct PN field.)
SQ

Sequence 120 AA;

Query Match 63.6%; Score 35; DB 16; Length 120;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVSLLRAYAMD 10
||:|||||
DB 99 RVTATLYAMD 108

RESULT 13

AAV91067
AAV91067 standard; Protein; 424 AA.

AAV91067;

DT 08-SEP-2000 (first entry)

DE Streptomyces nogalater nogalamycin biosynthesis ORF snoge protein.

XX Streptomyces nogalater; nogalamycin biosynthesis; antibiotic;

KW anthracycline biosynthetic pathway; gene cluster; drug screening;

KW antibiotic; anticancer antibiotic; anthracycline.

OS Streptomyces nogalater.

PN WO200024775-A1.

PD 04-MAY-2000.

PF 20-OCT-1999; 99WO-F100870.

PR 23-OCT-1998; 98FI-0002295.

PA (GALI-) GALILAEUS OY.
PI Ylinen K, Torkkell S, Palmu K, Hakala J;
XX

DR WPI; 2000-350696/30.
DR N-PSDB; AAA9283.

PT Isolated and purified DNA fragment for obtaining novel hybrid
PT antibiotics comprises the gene cluster for the anthracycline
PT biosynthetic pathway of the bacterium Streptomyces nogalater -

XX Example 1; Page 52-54; 59pp; English.

CC AAA9283 represents the nogalamycin biosynthesis gene cluster isolated
CC from Streptomyces nogalater. AAV91055 to AAV91071 represent ORF protein
CC sequences encoded by the gene cluster. Nogalamycin is an anthracycline
CC antibiotic, so the nogalamycin biosynthetic pathway is also known as the
CC anthracycline biosynthetic pathway. DNA fragments, plasmids and process
CC from the present invention are useful for obtaining novel hybrid
CC antibiotics, such as anthracyclines (anticancer antibiotics) or
CC anthracyclones.

SQ Sequence 424 AA;

Query Match 63.6%; Score 35; DB 21; Length 424;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVSLLRAYAMD 10
||:|||||
DB 2 RVLTLSPAMD 11

RESULT 14

AAV90540
AAV90540 standard; protein; 119 AA.

AAV90540;

DT 25-MAR-2003 (updated)

DT 20-OCT-1989 (first entry)

XX Immunoglobulin H chain variable region.

KW Immunoglobulin; H chain variable region; HIV.

OS Mus musculus.

PN EP327000-A.

PD 09-AUG-1989.

PF 30-JAN-1989; 89EP-0101583.

PR 30-JAN-1988; 88JP-0020255.

PR 08-JUL-1988; 88JP-0171385.

PA (KAGA) CEMO SERO THERAPEUTIC RES INS.

PI Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,
PI Taketsuki K;

DR WPI; 1989-229050/32.

DR N-PSDB; AAN90491, AAN90493, AAN90495.

PT Chimeric anti-human immune virus antibodies - contg. mouse variable
PT regions and human constant regions for diagnosis, treatment and
PT prevention of AIDS

XX Claim 2; page 14; 33pp; English.

CC The H chain variable region is from an immunoglobulin with anti-HIV
CC neutralising activity. See AAN90491, AAN90493 and AAN90495.

CC (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 119 AA;

Query Match 61.8%; Score 34; DB 10; Length 119;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAYAMDY 11
 : |||||
 DB 102 SAYAMDY 108

RESULT 15

AA24555
 ID AAR24555 standard; Protein; 119 AA.

XX AAR24555;

XX 08-DEC-1992 (first entry)

XX Human x mouse modified anti-HIV antibody Heavy chain.

XX Heavy; light; CDR; HIV; AIDS; FR; framework region.

XX Synthetic.

XX Key Location/Qualifiers

FT 1..29

FT /label= FR1

FT /note= "human antibody derived amino acid sequence"

FT 31..35

FT /label= CDR1

FT 41..47

FT /label= FR2

FT /note= "human antibody derived amino acid sequence"

FT 50..66

FT /label= CDR2

FT 73..97

FT /label= FR3

FT /note= "human antibody derived amino acid sequence"

FT 99..108

FT /label= CDR3

FT 109..119

FT /label= FR4

FT /note= "human antibody derived amino acid sequence"

XX JP04141095-A.

XX 14-MAY-1992.

XX 02-OCT-1990; 90JP-0266091.

XX 02-OCT-1990; 90JP-0266091.

XX (KAGA) KAGAKU OYOBI KESSEI RYOHO.

XX WPI; 1992-212765/26.

XX New recombinant modified anti-HIV antibodies - comprise human x

XX mouse modified antibody H and L chains

XX Claim 3; Page 1; 15pp; Japanese.

XX The human antibody derived amino acid sequence belongs to the human

XX antibody subgroup I. The CDRs and a part of the amino acid

XX sequence of the neighbouring framework region N- and/or C-terminal

XX are mouse monoclonal antibody derived sequences. The anti-HIV

XX modified antibody can be used for the prophylaxis and treatment of

XX AIDS.

XX Specific examples of the H chain are given in AAR24556-58 and

XX AAR24560-62. A specific example of the L chain is given in AAR24575.

XX Sequence 119 AA;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TAYAMDY 11
 : |||||
 DB 102 SAYAMDY 108

Search completed: September 10, 2003, 17:40:19
 Job time : 40.05 secs

Query Match 61.8%; Score 34; DB 13; Length 119;
 Best Local Similarity 85.7%; Pred. No. 35;